GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:28:46 ; Search time 114.5 Seconds
(without alignments)
736.365 Million cell updates/sec

Title: US-09-671-953B-5
Perfect score: 1132
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1130	99.8	218	4	AAB20358	Aab20358 Anti-chel
2	1118	98.8	218	4	AAB20359	Aab20359 Anti-chel
3	1113	98.3	218	4	AAB20360	Aab20360 Anti-chel
4	1079	95.3	218	8	ADQ98050	Adq98050 Chimeric
5	1078	95.2	218	8	ADQ98051	Adq98051 Chimeric
6	776	68.6	215	8	ADR23362	Adr23362 Human CD7
7	759	67.0	235	2	AAW82740	Aaw82740 Plasmid p
8	755.5	66.7	235	5	AAE27925	Aae27925 Human C2B
9	755.5	66.7	235	6	ABB82834	Abb82834 Antibody
10	755	66.7	213	8	ADL92471	Adl92471 Antibody
11	751	66.3	220	2	AAW07528	Aaw07528 Anti-HGF
12	750.5	66.3	235	3	AAB08025	Aab08025 A dimeric
13	749.5	66.2	234	5	AAO14066	Aao14066 Light cha
14	749.5	66.2	234	6	ABU08018	Abu08018 Human mon
15	749.5	66.2	234	7	ADF65776	Adf65776 Human mon
16	749.5	66.2	234	8	ADJ92516	Adj92516 Human SOJ
17	749	66.2	213	6	AAE34878	Aae34878 BIWA4/8 a
18	749	66.2	213	8	ADL15445	Adl15445 Humanised
19	749	66.2	213	8	ADO00853	Ado00853 Humanised
20	747	66.0	213	6	AAE35326	Aae35326 Humanised
21	747	66.0	213	6	AAE34877	Aae34877 BIWA4 ant
22	747	66.0	213	8	ADL15441	Adl15441 Humanised
23	747	66.0	213	8	ADO00849	Ado00849 Humanised
24	746	65.9	215	8	ADQ31891	Adq31891 Antibody
25	746	65.9	239	8	ADK70470	Adk70470 Respirato
26	745.5	65.9	240	6	ABJ38595	Abj38595 Hepatitis
27	744	65.7	215	8	ADQ31885	Adq31885 Antibody
28	742	65.5	215	8	ADQ16702	Adq16702 Modified
29	742	65.5	236	8	ADP79579	Adp79579 Chimeric
30	741.5	65.5	234	3	AAY92239	Aay92239 Human bon
31	741	65.5	236	2	AAY34096	Aay34096 Partial a
32	740	65.4	213	4	AAB83157	Aab83157 Gangliosi
33	740	65.4	233	3	AAY93704	Aay93704 The kappa
34	740	65.4	233	3	AAY93731	Aay93731 The kappa
35	740	65.4	233	6	AAE35886	Aae35886 Human 4.8
36	739.5	65.3	214	2	AAY08599	Aay08599 Anti-huma
37	739	65.3	241	6	ABJ38593	Abj38593 Hepatitis
38	738.5	65.2	234	6	ABP55483	Abp55483 CJRA05 pr
39	738.5	65.2	240	6	ABJ38594	Abj38594 Hepatitis
40	738	65.2	235	2	AAW06180	Aaw06180 Humanised
41	737.5	65.2	214	8	ADH34591	Adh34591 023 light
42	737	65.1	213	2	AAW05830	Aaw05830 Humanised
43	737	65.1	215	6	ABR01469	Abr01469 Human ant
44	736.5	65.1	216	8	ADS87940	Ads87940 Anti-IFN-
45	736.5	65.1	216	8	ADS94937	Ads94937 Anti-IFN-

ALIGNMENTS

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RESULT 1
AAB20358
ID   AAB20358 standard; protein; 218 AA.
XX
AC   AAB20358;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Anti-chelate antibody CHA255 light chain mutant N96C.
XX
KW   Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
KW   cancer; therapy; mutant; mutein.
XX
OS   Mus musculus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .23
FT                   /label= FR1
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FT   Region          24. .37
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FT                   /note= "complementarity determining region 1"
FT   Region          38. .52
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          53. .59
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          60. .92
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          93. .100
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Misc-difference 96
FT                   /note= "replaces Asn of wild-type sequence"
FT   Misc-difference 100
FT                   /note= "encoded by GTR"
FT   Region          101. .131
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FT   Misc-difference 112
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FT   Misc-difference 113
FT                   /note= "encoded by ACK"
FT   Misc-difference 206
FT                   /note= "encoded by AGY"
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FT   Misc-difference 207
FT                   /note= "encoded by TYG"
XX
PN   WO200122922-A2.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026619.
XX
PR   27-SEP-1999;   99US-0156194P.
PR   31-MAY-2000; 2000US-0208684P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Meares C,  Chmura A;
XX
DR   WPI; 2001-244971/25.
DR   N-PSDB; AAF30633.
XX
PT   Nucleic acid encoding a mutant antibody comprising a reactive site that
PT   specifically binds to a metal chelate useful as analytical agents and in
PT   clinical diagnosis, as well as in the treatment of disease, particularly
PT   cancer.
XX
PS   Disclosure; Fig 12; 100pp; English.
XX
CC   The invention provides a mutant antibody comprising a reactive site that
CC   is not present in the wild-type of the antibody. The antibody also has a
CC   complementarity determining region (CDR) that specifically binds to a
CC   metal chelate against which the wild-type antibody is raised. The
CC   reactive site of the mutant antibody is in a position proximate to or
CC   within the CDR, such that the chelate and the antibody are able to form a
CC   covalent bond. The present sequence is that of the light chain variable
CC   region of anti-indium-EDTA monoclonal antibody CHA255, carrying an N96C
CC   mutation. As an example of the method of the invention, rational computer
CC   -aided design was used to develop an indium-EDTA chelate to covalently
CC   bind to CHA255 in vivo. The premise was to allow the chelate to bind non-
CC   covalently to CHA255 bound to a tumour and then to covalently attach the
CC   chelate to the antibody, thereby trapping it at the tumour site. This
CC   involved cloning the variable domains of CHA255 to construct a
CC   human/mouse chimeric Fab fragment that could be expressed in Escherichia
CC   coli, and the synthesis and screening of benzyl-EDTA chelates carrying
CC   weakly electrophilic groups capable of conjugation of the antibody in
CC   vivo. This Fab can be conjugated to a targeting moiety when desired. A
CC   reactive site was incorporated into the antibody by engineering a Cys
CC   residue at location Asn-96 or Ser-95 of the light chain, near the region
CC   of the antibody to which the chelate bound. This was accomplished by site
CC   -directed mutagenesis of a nucleic acid encoding the wild-type of the
CC   anti-chelate antibody
XX
SQ   Sequence 218 AA;

  Query Match             99.8%;  Score 1130;  DB 4;  Length 218;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-80;
  Matches  218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
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Db          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60

Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
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Db         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||||||||||||
Db        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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RESULT 2
AAB20359
ID   AAB20359 standard; protein; 218 AA.
XX
AC   AAB20359;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Anti-chelate antibody CHA255 light chain.
XX
KW   Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
KW   cancer; therapy.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .23
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          24. .37
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          38. .52
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          53. .59
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          60. .92
FT                   /label= FR3
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FT   Region          93. .100
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FT                   /note= "complementarity determining region 3"
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FT                   /note= "encoded by GTR"
FT   Region          101. .131
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FT                   /note= "framework region 4"
FT   Misc-difference 112
FT                   /note= "encoded by CGW"
FT   Misc-difference 113
FT                   /note= "encoded by ACK"
FT   Misc-difference 206
FT                   /note= "encoded by AGY"
FT   Misc-difference 207
FT                   /note= "encoded by TYG"
XX
PN   WO200122922-A2.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026619.
XX
PR   27-SEP-1999;   99US-0156194P.
PR   31-MAY-2000; 2000US-0208684P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Meares C,  Chmura A;
XX
DR   WPI; 2001-244971/25.
DR   N-PSDB; AAF30634.
XX
PT   Nucleic acid encoding a mutant antibody comprising a reactive site that
PT   specifically binds to a metal chelate useful as analytical agents and in
PT   clinical diagnosis, as well as in the treatment of disease, particularly
PT   cancer.
XX
PS   Disclosure; Fig 13; 100pp; English.
XX
CC   The invention provides a mutant antibody comprising a reactive site that
CC   is not present in the wild-type of the antibody. The antibody also has a
```

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CC   complementarity determining region (CDR) that specifically binds to a
CC   metal chelate against which the wild-type antibody is raised. The
CC   reactive site of the mutant antibody is in a position proximate to or
CC   within the CDR, such that the chelate and the antibody are able to form a
CC   covalent bond. The present sequence is that of the light chain of anti-
CC   indium-EDTA monoclonal antibody CHA255. As an example of the method of
CC   the invention, rational computer-aided design was used to develop an
CC   indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was
CC   to allow the chelate to bind non-covalently to CHA255 bound to a tumour
CC   and then to covalently attach the chelate to the antibody, thereby
CC   trapping it at the tumour site. This involved cloning the variable
CC   domains of CHA255 to construct a human/mouse chimeric Fab fragment that
CC   could be expressed in Escherichia coli, and the synthesis and screening
CC   of benzyl-EDTA chelates carrying weakly electrophilic groups capable of
CC   conjugation of the antibody in vivo. This Fab can be conjugated to a
CC   targeting moiety when desired. A reactive site was incorporated into the
CC   antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the
CC   light chain, near the region of the antibody to which the chelate bound.
CC   This was accomplished by site-directed mutagenesis of a nucleic acid
CC   encoding the wild-type of the anti-chelate antibody
XX
SQ   Sequence 218 AA;

  Query Match             98.8%;  Score 1118;  DB 4;  Length 218;
  Best Local Similarity   99.5%;  Pred. No. 6.4e-79;
  Matches  217;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
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Db          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60

Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
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Db         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSNLWVFGGGTKLTVLSRTVAAPSVF 120

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218


RESULT 3
AAB20360
ID   AAB20360 standard; protein; 218 AA.
XX
AC   AAB20360;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Anti-chelate antibody CHA255 light chain mutant S95C.
XX
KW   Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
KW   cancer; therapy; mutant; mutein.
XX
OS   Mus musculus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .23
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FT                   /note= "framework region 1"
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FT                   /note= "complementarity determining region 2"
FT   Region          60. .92
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          93. .100
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Misc-difference 95
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FT                   /note= "encoded by GTR"
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FT                   /note= "encoded by CGW"
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FT                   /note= "encoded by ACK"
FT   Misc-difference 206
FT                   /note= "encoded by AGY"
FT   Misc-difference 207
FT                   /note= "encoded by TYG"
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PN   WO200122922-A2.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026619.
XX
PR   27-SEP-1999;   99US-0156194P.
PR   31-MAY-2000; 2000US-0208684P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Meares C,  Chmura A;
XX
DR   WPI; 2001-244971/25.
DR   N-PSDB; AAP30635.
XX
PT   Nucleic acid encoding a mutant antibody comprising a reactive site that
PT   specifically binds to a metal chelate useful as analytical agents and in
PT   clinical diagnosis, as well as in the treatment of disease, particularly
PT   cancer.
XX
PS   Disclosure; Fig 14; 100pp; English.
XX
CC   The invention provides a mutant antibody comprising a reactive site that
CC   is not present in the wild-type of the antibody. The antibody also has a
CC   complementarity determining region (CDR) that specifically binds to a
CC   metal chelate against which the wild-type antibody is raised. The
CC   reactive site of the mutant antibody is in a position proximate to or
CC   within the CDR, such that the chelate and the antibody are able to form a
CC   covalent bond. The present sequence is that of the light chain variable
CC   region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C
CC   mutation. As an example of the method of the invention, rational computer
CC   -aided design was used to develop an indium-EDTA chelate to covalently
CC   bind to CHA255 in vivo. The premise was to allow the chelate to bind non-
CC   covalently to CHA255 bound to a tumour and then to covalently attach the
CC   chelate to the antibody, thereby trapping it at the tumour site. This
CC   involved cloning the variable domains of CHA255 to construct a
CC   human/mouse chimeric Fab fragment that could be expressed in Escherichia
CC   coli, and the synthesis and screening of benzyl-EDTA chelates carrying
CC   weakly electrophilic groups capable of conjugation of the antibody in
CC   vivo. This Fab can be conjugated to a targeting moiety when desired. A
CC   reactive site was incorporated into the antibody by engineering a Cys
CC   residue at location Asn-96 or Ser-95 of the light chain, near the region
CC   of the antibody to which the chelate bound. This was accomplished by site
CC   -directed mutagenesis of a nucleic acid encoding the wild-type of the
CC   anti-chelate antibody
XX
SQ   Sequence 218 AA;

  Query Match             98.3%;  Score 1113;  DB 4;  Length 218;
  Best Local Similarity   99.1%;  Pred. No. 1.6e-78;
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Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
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Db         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218


RESULT 4
ADQ98050
ID   ADQ98050 standard; protein; 218 AA.
XX
AC   ADQ98050;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Chimeric murine 2D12.5 variable light chain fused to human TTCL protein.
XX
KW   murine; mouse; chimeric; human; TTCL; tetanus toxin;
KW   magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
KW   single photon emission tomography; SPET; cancer; cytostatic;
KW   immunosuppressive; multi-functional antibody; metal chelate;
KW   antigen recognition domain; in vivo imaging;
KW   cell-antibody-metal chelate complex; emission tomography.
XX
OS   Mus musculus.
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO2004065569-A2.
XX
PD   05-AUG-2004.
XX
PF   23-JAN-2004; 2004WO-US001808.
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PR   23-JAN-2003; 2003US-00350555.
PR   22-JUL-2003; 2003US-00625047.
PR   31-JUL-2003; 2003US-00631258.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Meares C,  Corneillie T;
XX
DR   WPI; 2004-580725/56.
DR   N-PSDB; ADQ98054.
XX
PT   Novel mutant antibody comprising reactive site not present in wild-type
PT   of antibody and antigen recognition domain that recognizes macrocyclic
PT   metal chelate having four nitrogen atoms, useful for treating cancer or
PT   autoimmune diseases.
XX
PS   Claim 41; SEQ ID NO 27; 208pp; English.
XX
CC   This invention relates to multi-functional antibodies that recognise
CC   chelating agents and metal chelates, particularly macrocyclic metal
CC   chelates. Specifically, it refers to an antibody that comprises a metal
CC   chelate bound to an antigen recognition domain, where the metal chelate
CC   has a reactive functional group of complementary reactivity to the
CC   reactive site of the antibody. This reactive site is the side chain of a
CC   naturally occurring amino acid e.g. the -SH group side chain of a
CC   cysteine residue (not present in the wild type) which can be used to form
CC   a covalent bond between the reactive site of the antibody and the
CC   reactive functional group of the metal chelate. The present invention
CC   describes using these antibodies for in vivo imaging where the antibody
CC   comprises a targeting moiety that binds specifically to a cell via a cell
CC   surface receptor or antigen thus forming a cell-mutant antibody complex.
CC   On addition of the metal chelate, a cell-antibody-metal chelate complex
CC   is formed that can be detected using emission tomography, magnetic
CC   resonance imaging, lanthanide luminescence, gamma-emissions or single
CC   photon emission tomography (SPET). As such, this method is useful for
CC   treating a subject with cancer and pharmaceutical compositions exhibit
CC   cytostatic and immunosuppressive activities. This polypeptide sequence is
CC   the chimeric murine antibody 2D12.5 variable light chain protein fused to
CC   the human anti-tetanus toxin antibody kappa light chain constant region
CC   of the invention.
XX
SQ   Sequence 218 AA;

  Query Match             95.3%;  Score 1079;  DB 8;  Length 218;
  Best Local Similarity   95.9%;  Pred. No. 6.8e-76;
  Matches  209;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

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Db          1 RSAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGNNNRPPG 60

Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
              |||||||||||||||| | |||||| ||||||||  ||||||||||||||||||||||||
Db         61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        181 STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218


RESULT 5
ADQ98051
ID   ADQ98051 standard; protein; 218 AA.
XX
AC   ADQ98051;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Chimeric N53C murine 2D12.5 light chain variable and human TTCL protein.
XX
KW   murine; mouse; chimeric; human; TTCL; tetanus toxin;
KW   magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
KW   single photon emission tomography; SPET; cancer; cytostatic;
KW   immunosuppressive; multi-functional antibody; metal chelate;
KW   antigen recognition domain; in vivo imaging;
KW   cell-antibody-metal chelate complex; emission tomography; mutant; mutein.
XX
OS   Mus musculus.
OS   Homo sapiens.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 55
FT                   /note= "Wild type Asn substituted for Cys"
XX
PN   WO2004065569-A2.
XX
PD   05-AUG-2004.
XX
PF   23-JAN-2004; 2004WO-US001808.
XX
PR   23-JAN-2003; 2003US-00350555.
PR   22-JUL-2003; 2003US-00625047.
PR   31-JUL-2003; 2003US-00631258.
XX
```

PA (REGC) UNIV CALIFORNIA.
XX
PI Meares C, Corneillie T;
XX
DR WPI; 2004-580725/56.
DR N-PSDB; ADQ98055.
XX
PT Novel mutant antibody comprising reactive site not present in wild-type
PT of antibody and antigen recognition domain that recognizes macrocyclic
PT metal chelate having four nitrogen atoms, useful for treating cancer or
PT autoimmune diseases.
XX
PS Claim 41; SEQ ID NO 28; 208pp; English.
XX
CC This invention relates to multi-functional antibodies that recognise
CC chelating agents and metal chelates, particularly macrocyclic metal
CC chelates. Specifically, it refers to an antibody that comprises a metal
CC chelate bound to an antigen recognition domain, where the metal chelate
CC has a reactive functional group of complementary reactivity to the
CC reactive site of the antibody. This reactive site is the side chain of a
CC naturally occurring amino acid e.g. the -SH group side chain of a
CC cysteine residue (not present in the wild type) which can be used to form
CC a covalent bond between the reactive site of the antibody and the
CC reactive functional group of the metal chelate. The present invention
CC describes using these antibodies for in vivo imaging where the antibody
CC comprises a targeting moiety that binds specifically to a cell via a cell
CC surface receptor or antigen thus forming a cell-mutant antibody complex.
CC On addition of the metal chelate, a cell-antibody-metal chelate complex
CC is formed that can be detected using emission tomography, magnetic
CC resonance imaging, lanthanide luminescence, gamma-emissions or single
CC photon emission tomography (SPET). As such, this method is useful for
CC treating a subject with cancer and pharmaceutical compositions exhibit
CC cytostatic and immunosuppressive activities. This polypeptide sequence is
CC the chimeric mutant N53C murine antibody 2D12.5 variable light chain
CC protein fused to the human anti-tetanus toxin antibody kappa light chain
CC constant region of the invention.
XX
SQ Sequence 218 AA;

Query Match 95.2%; Score 1078; DB 8; Length 218;
Best Local Similarity 95.9%; Pred. No. 8.2e-76;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
Qy          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
              |||||||||||||||||||||||||| |||||||||||||||||||||||| ||| ||
Db          1 RSAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGCNNRPPG 60

Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
              |||||||||||||||| | |||||| |||||||| ||||||||||||||||||||||||
Db         61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||| ||||||||||
Db        181 STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218
```

RESULT 6
ADR23362
ID ADR23362 standard; protein; 215 AA.
XX
AC ADR23362;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human CD72-targeted IgG1 light chain.
XX
KW Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;
KW immunosuppressive; cancer; autoimmune disease; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .109
FT /label= V_region
FT Region 110. .215
FT /label= C_region
XX
PN WO2004067569-A1.
XX
PD 12-AUG-2004.
XX
PF 27-JAN-2003; 2003WO-EP050004.
XX
PR 27-JAN-2003; 2003WO-EP050004.
XX
PA (CRUC-) CRUCELL HOLLAND BV.
XX
PI Bakker ABH, Marissen WE;
XX
DR WPI; 2004-580978/56.
DR N-PSDB; ADR23361.
XX
PT New internalizing human binding molecules capable of specifically binding
PT to CD72, useful for diagnosing and/or treating B-cell associated
PT diseases, such as cancer or autoimmune disorders.
XX
PS Example 5; SEQ ID NO 54; 174pp; English.
XX
CC The present sequence is the protein sequence of the light chain of human
CC IgG1 antibody 025, which specifically recognises human B cell associated
CC antigen CD72. An scFv ADR23324 selected from an antibody phage display
CC library was shown to specifically recognise the human CD72 receptor. The
CC scFv was recloned in IgG expression vector C01 using primers designed to
CC restore complete human frameworks, thereby generating antibody 025. Such
CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used
CC as internalising human binding molecules of the invention. These
CC internalising human binding molecules are capable of (specifically)
CC binding to CD72 or its antigenic determinant, and preferably bind to CD72
CC associated with cells. Upon binding to CD72 present on the surface of
CC target cells, the binding molecules internalise. In addition to the
CC internalising human binding molecules, the invention provides
CC immunoconjugates comprising an internalising human binding molecule and a
CC tag (toxic substance, radioactive substance, liposome and/or enzyme),
CC nucleic acids encoding these, and compositions comprising them. The
CC internalising human binding molecule, immunoconjugate, nucleic acid
CC molecule or composition can be used in the diagnosis and/or treatment of
CC a B cell associated disorder or disease, especially a B cell associated
CC cancer and B cell associated autoimmune disorder (claimed).
XX
SQ Sequence 215 AA;

Query Match 68.6%; Score 776; DB 8; Length 215;
Best Local Similarity 73.5%; Pred. No. 2.4e-52;
Matches 161; Conservative 16; Mismatches 36; Indels 6; Gaps 3;

```
Qy          2 SAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 61
              |: :||: |:: : |:|| :||:   |    | ||:| |:||      :| | |||  |:
Db          1 SSELTQDPAVSVALGQTVRITCQ---GDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGI 57

Qy         62 PARFSGSLIGDKAALTITGAQTEDEARYFCALWYSC--LWVFGGGTKLTVLSRTVAAPSV 119
              | |||||  |: |:|||||||| |||| |:|    |      |||||||||| |||||||
Db         58 PDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLG-TVAAPSV 116

Qy        120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176

Qy        180 SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||| ||||||||||
Db        177 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

```
RESULT 7
AAW82740
ID   AAW82740 standard; protein; 235 AA.
XX
AC   AAW82740;
XX
DT   10-MAY-1999  (first entry)
XX
DE   Plasmid pNG3/A5B7VK-HuCK-NEO protein.
XX
KW   Conjugate; cell targeting; cytotoxic drug; prodrug therapy system;
KW   prodrug-converting enzyme; cell surface antigen; treatment; cancer;
KW   inflammation; rheumatoid arthritis; antibody.
XX
OS   Synthetic.
XX
PN   WO9851787-A2.
XX
PD   19-NOV-1998.
XX
PF   05-MAY-1998;   98WO-GB001294.
XX
PR   10-MAY-1997;   97GB-00009421.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Emery SC,  Blakey DC;
XX
DR   WPI; 1999-059700/05.
DR   N-PSDB; AAV72047.
XX
PT   New gene construct expressing conjugate of targetting agent and prodrug-
PT   converting enzyme - useful for, e.g. targetted production of cytotoxic
PT   drug in vivo, especially for treatment of cancer.
XX
PS   Example 1f; Page 70; 100pp; English.
XX
CC   This sequence is used in a method for obtaining a novel gene construct
CC   (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-
CC   targeting group (I) and a heterologous prodrug-converting enzyme (II),
CC   and (B) is directed to leave the cell for selective localisation at a
CC   cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target
CC   site, then administration of (III) is used for targeted release of
CC   cytotoxic drug, specifically for treating cancer but also inflammation
CC   such as rheumatoid arthritis. In situ generation of the targeting
CC   antibody increases selectivity, reducing side effects at normal tissue.
CC   The method is applicable to any antibody-directed enzyme prodrug therapy
CC   system
XX
SQ   Sequence 235 AA;

  Query Match             67.0%;  Score 759;  DB 2;  Length 235;
  Best Local Similarity   72.2%;  Pred. No. 5.5e-51;
  Matches  156;  Conservative   15;  Mismatches   39;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |::|  | |: |||| ||:|||:|    ::  | :| |:||       |  |:| | |||
Db         25 VLSQSPAILSASPGEKVTMTCRAS----SSVTYIHWYQQKPGSSPKSWIYATSNLASGVP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |   :|||:  : || | |:|  | |    ||||||| :  ||||||||||
Db         81 ARFSGSGSGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 8
```

```
AAE27925
ID   AAE27925 standard; protein; 235 AA.
XX
AC   AAE27925;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human C2B8 antibody light chain protein.
XX
KW   Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
KW   neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
KW   non-Hodgkin's lymphoma; haematologic malignancy; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200260955-A2.
XX
PD   08-AUG-2002.
XX
PF   29-JAN-2002; 2002WO-US002373.
XX
PR   29-JAN-2001; 2001US-0264318P.
PR   16-NOV-2001; 2001US-0331481P.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Braslawsky GR,  Hanna N,  Chinn P;
XX
DR   WPI; 2002-698547/75.
DR   N-PSDB; AAD45754.
XX
PT   Novel domain deleted CC49 antibody reactive with tumor associated antigen
PT   -72, or C2B8 antibody reactive with CD20, useful for treating
PT   myelosuppressed patient suffering from a neoplastic disorder.
XX
PS   Example 1; Fig 3B; 74pp; English.
XX
CC   The present invention relates to domain deleted CC49 or C2B8 antibodies.
CC   Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
CC   deleted sequence in which CH2 domain has been deleted and are reactive
CC   with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
CC   with CD20 and comprise a heavy chain having a sequence of a derived
CC   domain deleted C2B8 construct where the CH2 domain has been deleted.
CC   Sequences of the invention are useful for imaging a neoplasm. They are
CC   also useful for treating myelosuppressed patients suffering from
CC   neoplastic disorder such as haematologic neoplasm, preferably non-
CC   Hodgkin's lymphoma. Antibodies of the invention are also used to treat
CC   neoplastic disorder, colon cancer and haematologic malignancy. They are
CC   useful for reducing tumour size, inhibiting tumour growth and/or
CC   prolonging the survival time of tumour-bearing animals and for treating
CC   tumours. The present sequence is human C2B8 light chain protein. This
CC   sequence is used in the exemplification of the invention
XX
SQ   Sequence 235 AA;

  Query Match             66.7%;  Score 755.5;  DB 5;  Length 235;
  Best Local Similarity   70.5%;  Pred. No. 1e-50;
  Matches  155;  Conservative   16;  Mismatches   42;  Indels    7;  Gaps    3;

Qy          1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              |  :|  :|   |: |||| ||:|||:|    :: :| :| |:||       |  |:| |
Db         21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLA 76

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS 118
               ||| |||||  |   :|||:  : || | |:|  | |    ||||||| :  |||||||
Db         77 SGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEI-KRTVAAPS 135

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||| ||||||||||
```

```
Db        196 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
```

RESULT 9
ABB82834
ID ABB82834 standard; protein; 235 AA.
XX
AC ABB82834;
XX
DT 31-MAR-2003 (first entry)
XX
DE Antibody C2B8 light chain.
XX
KW C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
KW thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
KW dermatological; immunosuppressive; antiinflammatory.
XX
OS Homo sapiens.
XX
PN WO200296948-A2.
XX
PD 05-DEC-2002.
XX
PF 29-JAN-2002; 2002WO-US002374.
XX
PR 29-JAN-2001; 2001US-0264318P.
PR 16-NOV-2001; 2001US-0331481P.
PR 21-DEC-2001; 2001US-0341858P.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Braslawsky GR, Hanna N, Chinn P, Hariharan K;
XX
DR WPI; 2003-140446/13.
DR N-PSDB; ABZ24018.
XX
PT Novel dimeric antibody useful for treating immune disorder and neoplastic
PT disorder, has several non-covalently associated monomeric subunits.
XX
PS Example 1; Fig 3B; 78pp; English.
XX
CC The invention relates to a dimeric antibody (I) comprising several
CC monomeric subunits, where the monomeric subunits are non-covalently
CC associated. (I) is useful for treating a disorder, especially immune
CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
CC resistant Hodgkin's disease high grade, low grade and intermediate grade
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
CC lymphoadenopathy, small lymphocytic, follicular, diffuse large cell,
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
CC detailed description of the various uses of (I)). The present sequence
CC represents the antibody C2B8 light chain
XX
SQ Sequence 235 AA;

```
  Query Match             66.7%;  Score 755.5;  DB 6;  Length 235;
  Best Local Similarity   70.5%;  Pred. No. 1e-50;
  Matches  155;  Conservative   16;  Mismatches   42;  Indels    7;  Gaps    3;

Qy          1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              |  :|  :|   |: |||| ||:|||:|    :: :| :| |:||       |  |:| |
Db         21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLA 76

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS 118
                ||| |||||  |   :|||:  : || | |:|  | |    ||||||| :  |||||||
Db         77 SGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEI-KRTVAAPS 135

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||| ||||||||||
Db        196 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
```

RESULT 10
ADL92471
ID ADL92471 standard; protein; 213 AA.
XX
AC ADL92471;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antibody "Rituximab" light chain sequence.
XX
KW cytostatic; antiinflammatory; cardiovascular; gene therapy; antibody; Fc;
KW agriculture; industrial application.
XX
OS Homo sapiens.
XX
PN WO2004029207-A2.
XX
PD 08-APR-2004.
XX
PF 26-SEP-2003; 2003WO-US030249.
XX
PR 27-SEP-2002; 2002US-0414433P.
PR 23-JAN-2003; 2003US-0442301P.
PR 02-MAY-2003; 2003US-0467606P.
PR 12-JUN-2003; 2003US-0477839P.
XX
PA (XENC-) XENCOR.
XX
PI Lazar GA, Chirino AJ, Dang W, Desjarlais JR, Doberstein SK;
PI Hayes RJ, Karki SB, Vafa O;
XX
DR WPI; 2004-316096/29.
XX
PT New optimized Fc variant antibody useful for diagnosing or treating
PT diseases (e.g. cancer, inflammation or cardiovascular diseases), in
PT research and in agricultural or industrial applications.
XX
PS Example 12; Fig 31a; 192pp; English.
XX
CC The invention relates to an antibody comprising an Fc variant portion
CC having an amino acid modification in the Fc region of the parent Fc
CC polypeptide, where the Fc variant modulates binding to an Fc-gamma-R
CC compared to the parent Fc polypeptide. The antibody may also be used in
CC research and in agricultural or industrial applications. This sequence
CC corresponds to the light chain of the antibody "Rituximab" as an example
CC of an antibody of the invention.
XX
SQ Sequence 213 AA;

```
  Query Match             66.7%;  Score 755;  DB 8;  Length 213;
  Best Local Similarity   71.8%;  Pred. No. 1e-50;
  Matches  155;  Conservative   16;  Mismatches   39;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |::|  | |: |||| ||:|||:|    :: :| :| |:||       |  |:| | |||
Db          3 VLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
                |||||  |   :|||:  : || | |:|  | |    ||||||| :  |||||||||||
Db         59 VRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177
```

```
Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
```

RESULT 11
AAW07528
ID AAW07528 standard; protein; 220 AA.
XX
AC AAW07528;
XX
DT 04-MAR-1997 (first entry)
XX
DE Anti-HGF receptor MAb 5D5 Fab light chain.
XX
KW Hepatocyte growth factor receptor; HGF; c-Met; antagonist;
KW monoclonal antibody; MAb; Fab; breast cancer; pancreas cancer;
KW colon cancer; lung cancer; therapy.
XX
OS Mus sp.
XX
PN WO9638557-A1.
XX
PD 05-DEC-1996.
XX
PF 31-MAY-1996; 96WO-US008094.
XX
PR 02-JUN-1995; 95US-00460368.
XX
PA (GETH) GENENTECH INC.
XX
PI Schwall RH, Tabor KH;
XX
DR WPI; 1997-034371/03.
DR N-PSDB; AAT43873.
XX
PT Hepatocyte growth factor receptor antagonist - specifically anti-c-Met
PT receptor monoclonal antibody 5D5 Fab, useful for mammalian cancer
PT treatment.
XX
PS Claim 12; Fig 1A; 69pp; English.
XX
CC 5D5 Fab comprises a light chain (AAW07528) and heavy chain (AAW07529) of
CC monoclonal antibody (MAb) 5D5, a murine MAb raised against the hepatocyte
CC growth factor (HGF) receptor (c-Met). The Fab can be obtd. by papain
CC digestion of the MAb or by recombinant methods utilising cDNA clones
CC (AAT43873-74) coding for the light and heavy chains. 5D5 Fab is an
CC antagonist of the HGF receptor and is useful for the diagnosis and
CC treatment of breast, pancreas, colon and lung cancer
XX
SQ Sequence 220 AA;

```
  Query Match             66.3%;  Score 751;  DB 2;  Length 220;
  Best Local Similarity   71.8%;  Pred. No. 2.1e-50;
  Matches  153;  Conservative   14;  Mismatches   42;  Indels    4;  Gaps    2;

Qy          9 SALTTSPGETVTLTCRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAPGVPARF 65
              |:|| | || ||::|:||   : ||   ||  | |:||      ||   : |  ||| ||
Db          9 SSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRF 68

Qy         66 SGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
              :||  |    ||||  : :| | |:|  :|:  | ||||||| :  ||||||||||||||
Db         69 TGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEI-KRTVAAPSVFIFPPS 127

Qy        126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 187

Qy        186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||| ||||||||||
Db        188 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
```

RESULT 12
AAB08025
ID AAB08025 standard; protein; 235 AA.
XX
AC AAB08025;
XX
DT 12-SEP-2003 (revised)
DT 14-NOV-2000 (first entry)
XX
DE A dimeric anti-CD20 light chain polypeptide.
XX
KW Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;
KW complement system; Fcgamma receptor; cytotoxic effector cell;
KW host immune cell; programmed cell death; allergic disorder; cancer;
KW autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease;
KW allergic bronchopulmonary aspergillosis; allergic rhinitis;
KW Graves's disease; food allergy; allergic contact dermatitis; cancer;
KW B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis;
KW pigeon breeder's disease; hepatitis; leprosy; Lyme disease;
KW diabetes mellitus; candidiasis; aplastic anaemia.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FH Key   Location/Qualifiers
FT Peptide   1. .22
FT   /note= "signal peptide"
FT Protein   23. .128
FT   /note= "murine anti-human CD20 variable light chain"
FT Protein   129. .235
FT   /note= "human kappa light chain constant region"
XX
PN WO200044788-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US001893.
XX
PR 28-JAN-1999; 99US-00238741.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Braslawsky GR, Hanna N, Hariharan K, Labarre MJ, Huynh TB;
XX
DR WPI; 2000-514811/46.
DR N-PSDB; AAA63530.
XX
PT Genetically engineering immunoglobulin (Ig) G/IgG dimers for the
PT treatment of cancers, allergic disorders and autoimmune conditions.
XX
PS Example 1; Fig 1A-B; 65pp; English.
XX
CC The present sequence represents a dimeric anti-CD20 light chain
CC polypeptide. The dimeric immunoglobulin is used in the method of the
CC invention. The specification describes a method for producing an
CC immunoglobulin (Ig) G/IgG dimer. The method comprises genetically
CC engineering a monoclonal antibody to introduce a cysteine molecule which
CC inhibits formation of intramolecular disulphide bridges between sister
CC heavy chains on the same antibody molecule. The dimer is a homodimer or
CC heterodimer that is capable of activating components of the complement
CC system, and has the ability to activate and kill cells via the complement
CC cascade. The dimer is also capable of binding to Fcgamma receptors on
CC cytotoxic effector cells and on host immune cells, and is capable of
CC initiating programmed cell death. The IgG/IgG dimers may be used to treat
CC allergic disorders, cancers and autoimmune diseases such as allergic
CC asthma, allergic bronchopulmonary aspergillosis, allergic rhinitis,
CC atopic dermatitis, Crohn's disease, Graves's disease, food allergies,
CC allergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They
CC may also be used to treat a range of other diseases and disorders such as
CC rheumatoid arthritis, ulcerative colitis, psoriasis, pigeon breeder's
CC disease, hepatitis, leprosy, Lyme disease, diabetes mellitus, candidiasis

```
CC   and aplastic anaemia. They are also useful for inducing hyper-cross-
CC   linking of membrane antigens and for the preferential killing of selected
CC   cell populations. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ   Sequence 235 AA;

  Query Match             66.3%;  Score 750.5;  DB 3;  Length 235;
  Best Local Similarity   70.0%;  Pred. No. 2.5e-50;
  Matches  154;  Conservative   16;  Mismatches   43;  Indels    7;  Gaps    3;

Qy          1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              |  :|  :|   |: |||| ||:|||:|    :: :| :| |:||       |  |:| |
Db         21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKRWIYATSNLA 76

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS 118
               ||| |||||  |   :|||:  : || | |:|  | |    |||| || :  |||||||
Db         77 SGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGAKLEI-KRTVAAPS 135

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||| ||||||||||
Db        196 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 13
AAO14066
ID   AAO14066 standard; protein; 234 AA.
XX
AC   AAO14066;
XX
DT   07-MAY-2002  (first entry)
XX
DE   Light chain protein of the monoclonal antibody from clone JA.
XX
KW   HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain;
KW   human monoclonal rabies virus neutralising antibody; immunoglobulin;
KW   light chain; central nervous system; CNS; prophylactic therapy; clone JA.
XX
OS   Homo sapiens.
XX
PN   WO200188132-A2.
XX
PD   22-NOV-2001.
XX
PF   04-MAY-2001; 2001WO-US014468.
XX
PR   16-MAY-2000; 2000US-0204518P.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Hooper DC,  Dietzschold B;
XX
DR   WPI; 2002-062381/08.
DR   N-PSDB; AAK98702.
XX
PT   Novel isolated human monoclonal rabies virus neutralizing antibody useful
PT   for treating individual exposed to rabies virus and for preventing spread
PT   of rabies virus to central nervous system.
XX
PS   Claim 4; Page 24-25; 25pp; English.
XX
CC   This sequence represents the light chain protein of the monoclonal
CC   antibody from clone JA. The invention relates to an isolated human
CC   monoclonal rabies virus neutralising antibody (virucide) derived from
CC   cDNA clones encoding the antibody heavy and light chains expressed in
CC   heterologous expression systems and purified away from deleterious
CC   contaminants. The invention provides a fused gene encoding a chimeric
CC   immunoglobulin light chain and a fused gene encoding a chimeric
CC   immunoglobulin heavy chain. The antibody of the invention is useful for
CC   treating an individual exposed to a rabies virus by administering to the
CC   individual a therapeutically effective amount of the antibody, and
CC   preventing a spread of the rabies virus to the central nervous system
CC   (CNS). The antibody of the invention provides a safe and efficacious post
CC   -exposure prophylactic therapy for individuals exposed to a rabies virus
XX
SQ   Sequence 234 AA;

  Query Match             66.2%;  Score 749.5;  DB 5;  Length 234;
  Best Local Similarity   71.8%;  Pred. No. 3e-50;
  Matches  155;  Conservative   13;  Mismatches   43;  Indels    5;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  || ||:|    | | |  | |:||      ||  |:||| |:|
Db         23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||   |    |:|:  : || | |:|   ::  | || |||:    ||||||||||
Db         80 ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF 138

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 14
ABU08018
ID   ABU08018 standard; protein; 234 AA.
XX
AC   ABU08018;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Human monoclonal rabies virus antibody light chain, clone JH, protein.
XX
KW   Human; antibody; constant region; monoclonal antibody 57; Mab 57;
KW   variable region; Rabies; neurological disease; infection;
KW   central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;
KW   pathogen; vaccine; virucide; light chain.
XX
OS   Homo sapiens.
XX
PN   WO2003016501-A2.
XX
PD   27-FEB-2003.
XX
PF   21-AUG-2002; 2002WO-US026584.
XX
PR   21-AUG-2001; 2001US-0314023P.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Hooper DC,  Dietzschold B;
XX
DR   WPI; 2003-278566/27.
DR   N-PSDB; ABX12856.
XX
PT   New recombinant antibody comprising a constant region of Mab 57 linked to
PT   a non-Mab 57 variable region, useful for treating an individual exposed
PT   to a pathogen, e.g. rabies infection.
XX
PS   Example 1; Page 33-34; 38pp; English.
XX
CC   The invention discloses a recombinant antibody comprising a constant
CC   region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable
CC   region. Rabies is an acute, neurological disease caused by infection of
CC   the central nervous system with the rabies virus, a member of the
CC   Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods
CC   for producing an isolated recombinant antibody by culturing a host cell,
CC   containing a recombinant expression vector comprising the nucleic acid
```

CC molecule encoding the antibody, and isolating the recombinant antibody
CC expressed and treating an individual exposed to a pathogen by
CC administering to the individual the recombinant antibody. The recombinant
CC antibodies are useful for preventing (vaccine) and treating an individual
CC exposed to a pathogen, e.g. rabies infection. They are also useful for
CC the qualitative and quantitative determination of the rabies virus. The
CC sequences presented are the antibody protein fragments, the nucleic acids
CC encoding them or the PCR primers used to construct the recombinant
CC expression vector
XX
SQ Sequence 234 AA;

Query Match 66.2%; Score 749.5; DB 6; Length 234;
Best Local Similarity 71.8%; Pred. No. 3e-50;
Matches 155; Conservative 13; Mismatches 43; Indels 5; Gaps 3;

```
Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  || ||:|    | | |  | |:||      ||  |:||| |:|
Db         23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |:|:  : || | |:|   ::  | || |||:    ||||||||||
Db         80 ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF 138

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
```

RESULT 15
ADF65776
ID ADF65776 standard; protein; 234 AA.
XX
AC ADF65776;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human monoclonal rabies virus antibody light chain.
XX
KW Immunoglobulin; Ig; heavy chain; light chain; human;
KW monoclonal rabies virus neutralising antibody; rabies virus protein;
KW neuronal tissue; antirabies.
XX
OS Homo sapiens.
XX
PN US2003157112-A1.
XX
PD 21-AUG-2003.
XX
PF 21-AUG-2002; 2002US-00225108.
XX
PR 16-MAY-2000; 2000US-0204518P.
PR 04-MAY-2001; 2001US-00848832.
PR 21-AUG-2001; 2001US-0314023P.
XX
PA (HOOP/) HOOPER D C.
PA (DIET/) DIETZSCHOLD B.
XX
PI Hooper DC, Dietzschold B;
XX
DR WPI; 2003-777974/73.
DR N-PSDB; ADF65790.
XX
PT New isolated nucleic acid molecule encoding a sequence that neutralizes
PT an antibody that binds to rabies virus protein, useful for diagnosing,
PT preventing or treating infection of pathogens that target neuronal
PT tissues, e.g. rabies.
XX
PS Claim 2; SEQ ID NO 4; 22pp; English.
XX
CC The present invention relates to the isolation of immunoglobulin (Ig)
CC heavy and light chains of human monoclonal rabies virus neutralising
CC antibody, and the polynucleotide sequences encoding them. The antibody
CC specifically binds to a rabies virus protein. Also disclosed is a fused
CC gene encoding a chimeric immunoglobulin light or heavy chain comprising a
CC first DNA sequence encoding an immunoglobulin light or heavy chain
CC variable region of a monoclonal rabies virus neutralising antibody
CC produced by a heterohybridoma cell line and a second DNA sequence
CC encoding a human light or heavy chain constant region, and methods of
CC producing a recombinant antibody. The polynucleotide sequences,
CC antibodies and methods are useful for diagnosing, preventing or treating
CC an infection of pathogens that target neuronal tissues, particularly
CC rabies. The present sequence represents human monoclonal rabies virus
CC antibody light chain.
XX
SQ Sequence 234 AA;

Query Match 66.2%; Score 749.5; DB 7; Length 234;
Best Local Similarity 71.8%; Pred. No. 3e-50;
Matches 155; Conservative 13; Mismatches 43; Indels 5; Gaps 3;

```
Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  || ||:|    | | |  | |:||      ||  |:||| |:|
Db         23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |:|:  : || | |:|   ::  | || |||:    ||||||||||
Db         80 ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF 138

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
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Search completed: June 7, 2005, 15:54:03
Job time : 117.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:42:01 ; Search time 29.5 Seconds
(without alignments)
551.644 Million cell updates/sec

Title: US-09-671-953B-5
Perfect score: 1132
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	759	67.0	235	3	US-09-423-439-18	Sequence 18, Appl
2	751	66.3	220	3	US-08-952-235-1	Sequence 1, Appli
3	751	66.3	220	4	US-09-669-971-1	Sequence 1, Appli
4	740	65.4	233	4	US-09-472-087-15	Sequence 15, Appl
5	740	65.4	233	4	US-09-472-087-67	Sequence 67, Appl
6	738	65.2	235	4	US-09-011-769A-27	Sequence 27, Appl
7	735	64.9	213	3	US-08-397-411-12	Sequence 12, Appl
8	734.5	64.9	491	4	US-10-011-125A-2	Sequence 2, Appli
9	734	64.8	236	4	US-09-315-926A-79	Sequence 79, Appl
10	732	64.7	235	4	US-09-472-087-14	Sequence 14, Appl
11	732	64.7	235	4	US-09-472-087-65	Sequence 65, Appl
12	730.5	64.5	214	4	US-09-472-087-71	Sequence 71, Appl
13	730.5	64.5	224	4	US-09-456-090A-84	Sequence 84, Appl
14	730.5	64.5	224	4	US-09-453-234-84	Sequence 84, Appl
15	729.5	64.4	234	4	US-09-472-087-17	Sequence 17, Appl
16	729.5	64.4	234	4	US-09-472-087-69	Sequence 69, Appl
17	728.5	64.4	224	4	US-09-456-090A-46	Sequence 46, Appl
18	728.5	64.4	224	4	US-09-453-234-46	Sequence 46, Appl
19	728.5	64.4	234	4	US-09-740-002-24	Sequence 24, Appl
20	728	64.3	214	1	US-08-458-516-12	Sequence 12, Appl
21	727	64.2	233	3	US-09-485-737B-69	Sequence 69, Appl
22	727	64.2	233	4	US-10-071-485-69	Sequence 69, Appl
23	726	64.1	235	3	US-09-171-945-17	Sequence 17, Appl
24	725.5	64.1	224	4	US-09-456-090A-36	Sequence 36, Appl
25	725.5	64.1	224	4	US-09-453-234-36	Sequence 36, Appl
26	725.5	64.1	226	4	US-09-456-090A-74	Sequence 74, Appl
27	725.5	64.1	226	4	US-09-453-234-74	Sequence 74, Appl
28	724.5	64.0	214	3	US-09-247-352-4	Sequence 4, Appli
29	724.5	64.0	214	4	US-09-466-635-4	Sequence 4, Appli
30	723.5	63.9	213	3	US-08-630-820-6	Sequence 6, Appli
31	723.5	63.9	213	4	US-09-273-453-6	Sequence 6, Appli
32	723.5	63.9	236	1	US-08-157-101A-5	Sequence 5, Appli
33	723	63.9	219	3	US-09-027-449-72	Sequence 72, Appl
34	723	63.9	219	3	US-09-026-985-72	Sequence 72, Appl
35	723	63.9	219	4	US-09-121-952A-72	Sequence 72, Appl
36	723	63.9	219	4	US-09-234-340A-72	Sequence 72, Appl
37	723	63.9	239	4	US-09-627-896B-22	Sequence 22, Appl
38	723	63.9	242	3	US-09-027-449-56	Sequence 56, Appl
39	723	63.9	242	3	US-08-804-444A-56	Sequence 56, Appl
40	723	63.9	242	3	US-09-026-985-56	Sequence 56, Appl
41	723	63.9	242	4	US-09-121-952A-56	Sequence 56, Appl
42	723	63.9	242	4	US-09-234-340A-56	Sequence 56, Appl
43	722.5	63.8	214	3	US-08-397-411-5	Sequence 5, Appli
44	722	63.8	214	2	US-07-934-373C-24	Sequence 24, Appl
45	722	63.8	214	3	US-08-437-642B-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-423-439-18
; Sequence 18, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18

Query Match 67.0%; Score 759; DB 3; Length 235;
Best Local Similarity 72.2%; Pred. No. 1.6e-67;
Matches 156; Conservative 15; Mismatches 39; Indels 6; Gaps 3;

```
Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |::|  | |: |||| ||:|||:|    ::  | :| |:||       |  |:| | |||
Db         25 VLSQSPAILSASPGEKVTMTCRAS----SSVTYIHWYQQKPGSSPKSWIYATSNLASGVP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |   :|||:  : || | |:|  | |   ||||||| :  ||||||||||
```

```
Db         81 ARFSGSGSGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 2
US-08-952-235-1
; Sequence 1, Application US/08952235
; Patent No. 6207152
;  GENERAL INFORMATION:
;    APPLICANT:  Schwall, Ralph H.
;    APPLICANT:  Tabor, Kelly H.
;    TITLE OF INVENTION:  Hepatocyte Growth Factor Receptor
;    TITLE OF INVENTION:  Antagonists and Uses Thereof
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/952,235
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/460368
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marschang, Diane L.
;      REGISTRATION NUMBER:  35,600
;      REFERENCE/DOCKET NUMBER:  P0938P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5416
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  220 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-952-235-1

  Query Match             66.3%;  Score 751;  DB 3;  Length 220;
  Best Local Similarity   71.8%;  Pred. No. 9.2e-67;
  Matches  153;  Conservative   14;  Mismatches   42;  Indels    4;  Gaps    2;

Qy          9 SALTTSPGETVTLTCRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAPGVPARF 65
              |:|| | || ||::|:||   : ||   ||  | |:||      ||   : |  ||| ||
Db          9 SSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRF 68

Qy         66 SGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
                :||  |    ||||  : :| | |:|  :|:  | ||||||| :  ||||||||||||||
Db         69 TGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEI-KRTVAAPSVFIFPPS 127

Qy        126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 187

Qy        186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        188 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220


RESULT 3
US-09-669-971-1
; Sequence 1, Application US/09669971
; Patent No. 6468529
;  GENERAL INFORMATION:
;       APPLICANT: Schwall, Ralph H.
;                  Tabor, Kelly H.
;       TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
;                           Antagonists and Uses Thereof
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/669,971
;            FILING DATE: 05-Jul-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/952,235
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/460368
;            FILING DATE: 02-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Marschang, Diane L.
;            REGISTRATION NUMBER: 35,600
;            REFERENCE/DOCKET NUMBER: P0938P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-5416
;            TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 220 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-669-971-1

  Query Match             66.3%;  Score 751;  DB 4;  Length 220;
  Best Local Similarity   71.8%;  Pred. No. 9.2e-67;
  Matches  153;  Conservative   14;  Mismatches   42;  Indels    4;  Gaps    2;

Qy          9 SALTTSPGETVTLTCRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAPGVPARF 65
              |:|| | || ||::|:||   : ||   ||  | |:||      ||   : |  ||| ||
Db          9 SSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRF 68

Qy         66 SGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
                :||  |    ||||  : :| | |:|  :|:  | ||||||| :  ||||||||||||||
Db         69 TGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEI-KRTVAAPSVFIFPPS 127

Qy        126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 187

Qy        186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        188 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220


RESULT 4
US-09-472-087-15
; Sequence 15, Application US/09472087
; Patent No. 6682736
```

```
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-15

  Query Match             65.4%;  Score 740;  DB 4;  Length 233;
  Best Local Similarity   70.4%;  Pred. No. 1.2e-65;
  Matches  152;  Conservative   18;  Mismatches   40;  Indels    6;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||  ||:||:|:    :|:|  | |:||       || | ::|| |:|
Db         23 VLTQSPGTLSLSPGERATLSCRTSV----SSSYLAWYQQKPGQAPRLLIYGASSRATGIP 78

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
               |||||  |    |||:  : || | |:|  :    : ||||||: :  ||||||||||
Db         79 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGISPFTFGGGTKVEI-KRTVAAPSVFIF 137

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 197

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        198 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 233


RESULT 5
US-09-472-087-67
; Sequence 67, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-67

  Query Match             65.4%;  Score 740;  DB 4;  Length 233;
  Best Local Similarity   70.4%;  Pred. No. 1.2e-65;
  Matches  152;  Conservative   18;  Mismatches   40;  Indels    6;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||  ||:||:|:    :|:|  | |:||       || | ::|| |:|
Db         23 VLTQSPGTLSLSPGERATLSCRTSV----SSSYLAWYQQKPGQAPRLLIYGASSRATGIP 78

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
               |||||  |    |||:  : || | |:|  :    : ||||||: :  ||||||||||
Db         79 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGISPFTFGGGTKVEI-KRTVAAPSVFIF 137

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 197

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        198 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 233


RESULT 6
US-09-011-769A-27
; Sequence 27, Application US/09011769A
; Patent No. 6436691
;  GENERAL INFORMATION:
;       APPLICANT: SLATER, Anthony M.
;                  BLAKEY, David C.
;                  DAVIES, David H.
;                  HENNAM, John F.
;                  HENNEQUIN, Laurent F.A.
;                  MARSHAM, Peter R.
;                  DOWELL, Robert I.
;       TITLE OF INVENTION: Chemical Compounds
;       NUMBER OF SEQUENCES: 87
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pillsbury Madison & Sutro, LLP
;            STREET: 1100 New York Ave., N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: U.S.A.
;            ZIP: 20005
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 1.44 Mb disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: MS Word
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/011,769A
;            FILING DATE: 13-Feb-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/GB96/01975
;            FILING DATE: 13-AUG-1996
;            APPLICATION NUMBER: GB 9612295.7
;            FILING DATE: 12-JUN-1996
;            APPLICATION NUMBER: GB 9611019.2
;            FILING DATE: 25-MAY-1996
;            APPLICATION NUMBER: GB 9516810.0
;            FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 27:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 235 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-011-769A-27

  Query Match             65.2%;  Score 738;  DB 4;  Length 235;
  Best Local Similarity   71.3%;  Pred. No. 2e-65;
  Matches  154;  Conservative   15;  Mismatches   41;  Indels    6;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  |:|: | |: ||:|||:|    ::  | :| |:||       | |:| | |||
Db         25 VLTQSPSSLSVSVGDRVTMTCRAS----SSVTYIHWYQQKPGLAPKSWIYATSNLASGVP 80
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Qy          63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
               :|||||  |    |||:  | || | |:|  | |    || |||: |  ||||||||||
Db          81 SRFSGSGSGTDYTLTISSLQPEDIATYYCQHWSSKPPTFGQGTKVEV-KRTVAAPSVFIF 139

Qy         123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy         183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
               |||||||||||||||||||| ||||||||||
Db         200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 7
US-08-397-411-12
; Sequence 12, Application US/08397411
; Patent No. 6129914
;  GENERAL INFORMATION:
;    APPLICANT:  Weiner, George
;    APPLICANT:  Gingrich, Roger
;    APPLICANT:  Link, Brian
;    APPLICANT:  Tso, J. Yun
;    TITLE OF INVENTION:  Bispecific Antibody Effective to Treat
;    TITLE OF INVENTION:  B-Cell Lymphoma and Cell Line
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/397,411
;      FILING DATE:  01-MAR-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/859,583
;      FILING DATE:  27-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  011823-004901
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  213 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-397-411-12

  Query Match             64.9%;  Score 735;  DB 3;  Length 213;
  Best Local Similarity   70.7%;  Pred. No. 3.4e-65;
  Matches  152;  Conservative   16;  Mismatches   41;  Indels    6;  Gaps    3;

Qy           5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
               :||  |:|: | |: ||:|| :|    :: :| || |:||      ||  |:  | |||:
Db           4 MTQSPSSLSASVGDRVTITCSAS----SSVSYMNWYQQKPGKAPKRLIYDTSKLASGVPS 59

Qy          64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
               |||||  |    |||:  | ||   |:|  | |    ||||||: :  ||||||||||||
Db          60 RFSGSGSGTDFTLTISSLQPEDFDTYYCQQWSSNPPTFGGGTKVEI-KRTVAAPSVFIFP 118

Qy         124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         119 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 178

Qy         184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
               |||||||||||||||||||| ||||||||||
Db         179 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213


RESULT 8
US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
;  APPLICANT: Chen, Christina Yu-Ching
;  TITLE OF INVENTION: BACTERIAL HOST STRAINS
;  FILE REFERENCE: P1804R1
;  CURRENT APPLICATION NUMBER: US/10/011,125A
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: US 60/256,162
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2

  Query Match             64.9%;  Score 734.5;  DB 4;  Length 491;
  Best Local Similarity   70.7%;  Pred. No. 1.2e-64;
  Matches  152;  Conservative   16;  Mismatches   42;  Indels    5;  Gaps    3;

Qy           5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
               :||  |:|: | |: ||:|| :|      ||| || |:||      ||  |::   |||:
Db          27 LTQSPSSLSASVGDRVTITCSAS---QDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 83

Qy          64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
               |||||  |    |||:  | ||  | |:|  : :  | || |||: :  ||||||||||||
Db          84 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEI-KRTVAAPSVFIFP 142

Qy         124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         143 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 202

Qy         184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
               |||||||||||||||||||| ||||||||||
Db         203 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237


RESULT 9
US-09-315-926A-79
; Sequence 79, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
;  APPLICANT: Es van, Helmuth
;  APPLICANT:  Havenga, Menzo
;  APPLICANT:  Verlinden, Stefan
;  TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
;  FILE REFERENCE: 2183-4080US
;  CURRENT APPLICATION NUMBER: US/09/315,926A
;  CURRENT FILING DATE:  1999-05-20
;  PRIOR APPLICATION NUMBER: EP 99201593.3
;  PRIOR FILING DATE: 1999-05-20
;  PRIOR APPLICATION NUMBER: EP 98201693.3
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Description of Artificial Sequence: phage
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(236)
;   OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-79

  Query Match             64.8%;  Score 734;  DB 4;  Length 236;
  Best Local Similarity   72.6%;  Pred. No. 4.9e-65;
  Matches  151;  Conservative   13;  Mismatches   42;  Indels    2;  Gaps    2;

Qy         11 LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPARFSGSLI 70
              |: |||   ||:||:|  :|:: | | | |:||      || | :||| ||| |||||
Db         31 LSLSPGAGATLSCRAS-QSVSSRNLA-WYQQKPGQAPRLLIYGVSNRATGVPDRFSGSGS 88

Qy         71 GDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPSDEQLK 130
              |    |||   : || | |:|  :   || || |||: :  ||||||||||||||||||
Db         89 GADFTLTINRLEPEDFAVYYCQRYGRSLWTFGQGTKVEIKRGTVAAPSVFIFPPSDEQLK 148

Qy        131 SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY 208

Qy        191 EKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||| ||||||||||
Db        209 EKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 10
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-14

  Query Match             64.7%;  Score 732;  DB 4;  Length 235;
  Best Local Similarity   69.4%;  Pred. No. 7.8e-65;
  Matches  150;  Conservative   19;  Mismatches   43;  Indels    4;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||  ||:||:|     :|::  | |::|       || | ::|| |:|
Db         23 VLTQSPGTLSLSPGERATLSCRAS--QSISSSFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
               |||||  |    |||:  : || | |:|  : :  | || |||: :  ||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPWTFGQGTKVEI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 11
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-65

  Query Match             64.7%;  Score 732;  DB 4;  Length 235;
  Best Local Similarity   69.4%;  Pred. No. 7.8e-65;
  Matches  150;  Conservative   19;  Mismatches   43;  Indels    4;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
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Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPWTFGQGTKVEI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
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Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 12
US-09-472-087-71
; Sequence 71, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
;   LENGTH: 214
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-09-472-087-71

  Query Match             64.5%;  Score 730.5;  DB 4;  Length 214;
  Best Local Similarity   69.8%;  Pred. No. 9.7e-65;
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              :||  |:|: | |: ||:|||:|    : ::| :| |:||      ||   ::   |||:
Db          4 MTQSPSSLSASVGDRVTITCRAS---QSINSYLDWYQQKPGKAPKLLIYAASSLQSGVPS 60

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  |    |||:  | || | |:|  :||  : || |||: :  ||||||||||||
Db         61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTPFTFGPGTKVEI-KRTVAAPSVFIFP 119

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 179

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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RESULT 13
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-32L
US-09-456-090A-84

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Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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Db         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRNNWPLTFGGGTKVEI-KRTVAAPSVFIF 118

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 178

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGE 217
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Db        179 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213


RESULT 14
US-09-453-234-84
; Sequence 84, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-32L
US-09-453-234-84

  Query Match             64.5%;  Score 730.5;  DB 4;  Length 224;
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  Matches  153;  Conservative   15;  Mismatches   42;  Indels    5;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
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RESULT 15
US-09-472-087-17
; Sequence 17, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-17

  Query Match             64.4%;  Score 729.5;  DB 4;  Length 234;
  Best Local Similarity   69.9%;  Pred. No. 1.4e-64;
  Matches  151;  Conservative   17;  Mismatches   43;  Indels    5;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
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Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              |||||  |    |||:  : || | |:|  :    : || |||: :  ||||||||||
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Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
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Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
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Title: US-09-671-953B-5
Perfect score: 1132
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

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Searched: 1599520 seqs, 360203123 residues

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1079	95.3	218	16	US-10-625-047-27	Sequence 27, Appl
2	1078	95.2	218	16	US-10-625-047-28	Sequence 28, Appl
3	755.5	66.7	235	16	US-10-723-003-42	Sequence 42, Appl
4	751	66.3	220	9	US-09-995-693-1	Sequence 1, Appli
5	751	66.3	220	14	US-10-232-408-1	Sequence 1, Appli
6	749.5	66.2	234	10	US-09-848-832-4	Sequence 4, Appli
7	749.5	66.2	234	14	US-10-225-108A-4	Sequence 4, Appli
8	749.5	66.2	234	15	US-10-461-148-2	Sequence 2, Appli
9	749	66.2	213	14	US-10-150-475A-8	Sequence 8, Appli
10	749	66.2	213	16	US-10-704-522-8	Sequence 8, Appli
11	749	66.2	213	16	US-10-645-215-8	Sequence 8, Appli
12	747	66.0	213	14	US-10-150-475A-4	Sequence 4, Appli
13	747	66.0	213	16	US-10-704-522-4	Sequence 4, Appli
14	747	66.0	213	16	US-10-645-215-4	Sequence 4, Appli
15	742	65.5	215	15	US-10-307-724-122	Sequence 122, App
16	742	65.5	215	16	US-10-737-290-122	Sequence 122, App
17	742	65.5	239	16	US-10-737-290-142	Sequence 142, App
18	741	65.5	213	15	US-10-435-299-12	Sequence 12, Appl
19	740	65.4	233	14	US-10-153-382-11	Sequence 11, Appl
20	740	65.4	233	16	US-10-612-497-15	Sequence 15, Appl
21	740	65.4	233	16	US-10-612-497-67	Sequence 67, Appl
22	740	65.4	233	16	US-10-776-649-15	Sequence 15, Appl
23	740	65.4	233	16	US-10-776-649-67	Sequence 67, Appl
24	739	65.3	669	9	US-09-807-721-2	Sequence 2, Appli
25	738.5	65.2	234	15	US-10-045-674-587	Sequence 587, App
26	737	65.1	215	16	US-10-128-520-106	Sequence 106, App
27	736.5	65.1	234	15	US-10-292-088-88	Sequence 88, Appl
28	735.5	65.0	214	15	US-10-364-953-1	Sequence 1, Appli
29	735.5	65.0	237	14	US-10-020-786-10	Sequence 10, Appl
30	735.5	65.0	667	16	US-10-764-428-7	Sequence 7, Appli
31	735.5	65.0	667	16	US-10-764-428-13	Sequence 13, Appl
32	735.5	65.0	667	16	US-10-764-428-25	Sequence 25, Appl
33	735.5	65.0	670	16	US-10-764-428-5	Sequence 5, Appli
34	735.5	65.0	670	16	US-10-764-428-9	Sequence 9, Appli
35	735.5	65.0	670	16	US-10-764-428-11	Sequence 11, Appl
36	735.5	65.0	670	16	US-10-764-428-27	Sequence 27, Appl
37	735	64.9	235	15	US-10-656-769-38	Sequence 38, Appl
38	734.5	64.9	237	9	US-09-056-160B-100	Sequence 100, App
39	734.5	64.9	237	14	US-10-234-671-100	Sequence 100, App
40	734.5	64.9	491	13	US-10-011-125-2	Sequence 2, Appli
41	734	64.8	236	14	US-10-235-175-79	Sequence 79, Appl
42	733	64.8	215	15	US-10-408-901-40	Sequence 40, Appl
43	733	64.8	215	15	US-10-408-901-48	Sequence 48, Appl
44	733	64.8	215	15	US-10-408-901-52	Sequence 52, Appl
45	733	64.8	215	16	US-10-128-520-129	Sequence 129, App

ALIGNMENTS

RESULT 1
US-10-625-047-27
; Sequence 27, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Corneillie, Todd
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 02307O-130910US
; CURRENT APPLICATION NUMBER: US/10/625,047
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:native cloned
; OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region
; OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody
; OTHER INFORMATION: kappa light chain constant region (TTCL)
US-10-625-047-27

Query Match 95.3%; Score 1079; DB 16; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.8e-83;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

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Db        181 STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218


RESULT 2
US-10-625-047-28
; Sequence 28, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
;  APPLICANT: Meares, Claude
;  APPLICANT:  Corneillie, Todd
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Multi-Functional Antibodies
;  FILE REFERENCE: 02307O-130910US
;  CURRENT APPLICATION NUMBER: US/10/625,047
;  CURRENT FILING DATE:  2003-07-22
;  PRIOR APPLICATION NUMBER: US 10/350,555
;  PRIOR FILING DATE: 2003-01-23
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:N53C cloned
;   OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable
;   OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin
;   OTHER INFORMATION: antibody kappa light chain constant region (TTCL)
US-10-625-047-28

  Query Match             95.2%;  Score 1078;  DB 16;  Length 218;
  Best Local Similarity   95.9%;  Pred. No. 2.2e-83;
  Matches  209;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

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Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
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RESULT 3
US-10-723-003-42
; Sequence 42, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
;  APPLICANT: MA, Jing
;  APPLICANT:  GUO, Yajun
;  TITLE OF INVENTION: PREPARATION AND APPLICATION OF
;  TITLE OF INVENTION:  ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
;  FILE REFERENCE: 549062000200
;  CURRENT APPLICATION NUMBER: US/10/723,003
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: CN 2003101199300
;  PRIOR FILING DATE: 2003-11-25
;  PRIOR APPLICATION NUMBER: CN 031292909
;  PRIOR FILING DATE: 2003-06-13
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-723-003-42

  Query Match             66.7%;  Score 755.5;  DB 16;  Length 235;
  Best Local Similarity   70.5%;  Pred. No. 5.2e-56;
  Matches  155;  Conservative   16;  Mismatches   42;  Indels    7;  Gaps    3;

Qy          1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              |  :|  :|   |: |||| ||:|||:|    :: :| :| |:||        |  |:| |
Db         21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLA 76

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS 118
              ||| |||||  |   :|||:  : || | |:|  | |    ||||||| :  |||||||
Db         77 SGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEI-KRTVAAPS 135

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        196 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 4
US-09-995-693-1
; Sequence 1, Application US/09995693
; Patent No. US20020136721A1
;  GENERAL INFORMATION:
;       APPLICANT: Schwall, Ralph H.
;                  Tabor, Kelly H.
;       TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
;                           Antagonists and Uses Thereof
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/995,693
;            FILING DATE: 29-No. US20020136721A1-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/952,235
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Marschang, Diane L.
;            REGISTRATION NUMBER: 35,600
;            REFERENCE/DOCKET NUMBER: P0938P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-5416
;            TELEFAX: 650/952-9881
;  INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
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;             LENGTH: 220 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-995-693-1

  Query Match             66.3%;  Score 751;  DB 9;  Length 220;
  Best Local Similarity   71.8%;  Pred. No. 1.2e-55;
  Matches  153;  Conservative   14;  Mismatches   42;  Indels    4;  Gaps    2;

Qy          9 SALTTSPGETVTLTCRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAPGVPARF 65
              |:|| | || ||::|:||   : ||   ||  | |:||       ||   : |  ||| ||
Db          9 SSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRF 68

Qy         66 SGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
              :||  |    ||||  : :| | |:|  :|:  | ||||||| :  ||||||||||||||
Db         69 TGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEI-KRTVAAPSVFIFPPS 127

Qy        126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 187

Qy        186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        188 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220


RESULT 5
US-10-232-408-1
; Sequence 1, Application US/10232408
; Publication No. US20030118587A1
;   GENERAL INFORMATION:
;        APPLICANT: Schwall, Ralph H.
;                   Tabor, Kelly H.
;        TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
;                            Antagonists and Uses Thereof
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/232,408
;             FILING DATE: 03-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/669,971
;             FILING DATE: 05-Jul-2001
;             APPLICATION NUMBER: US/08/952,235
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/460368
;             FILING DATE: 02-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Marschang, Diane L.
;             REGISTRATION NUMBER: 35,600
;             REFERENCE/DOCKET NUMBER: P0938P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-5416
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 220 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-232-408-1

  Query Match             66.3%;  Score 751;  DB 14;  Length 220;
  Best Local Similarity   71.8%;  Pred. No. 1.2e-55;
  Matches  153;  Conservative   14;  Mismatches   42;  Indels    4;  Gaps    2;

Qy          9 SALTTSPGETVTLTCRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAPGVPARF 65
              |:|| | || ||::|:||   : ||   ||  | |:||       ||   : |  ||| ||
Db          9 SSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRF 68

Qy         66 SGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
              :||  |    ||||  : :| | |:|  :|:  | ||||||| :  ||||||||||||||
Db         69 TGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEI-KRTVAAPSVFIFPPS 127

Qy        126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 187

Qy        186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        188 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220


RESULT 6
US-09-848-832-4
; Sequence 4, Application US/09848832
; Publication No. US20030165507A1
; GENERAL INFORMATION:
;  APPLICANT: Hooper, Douglas
;  APPLICANT:  Dietzschold, Bernhard
;  TITLE OF INVENTION: RABIES VIRUS-SPECFIC NEUTRALIZING HUMAN
;  TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
;  FILE REFERENCE: HOO01.NP0002
;  CURRENT APPLICATION NUMBER: US/09/848,832
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: 60/204,518
;  PRIOR FILING DATE: 2000-05-16
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-848-832-4

  Query Match             66.2%;  Score 749.5;  DB 10;  Length 234;
  Best Local Similarity   71.8%;  Pred. No. 1.7e-55;
  Matches  155;  Conservative   13;  Mismatches   43;  Indels    5;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  || ||:|    | | |  | |:||       ||  |:||| |:|
Db         23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |:|:  : || | |:|   ::  | || |||:    ||||||||||
Db         80 ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF 138

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 7
US-10-225-108A-4
; Sequence 4, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
;  APPLICANT: HOOPER, Craig
;  APPLICANT:  DIETZSCHOLD, Bernhard
```

```
;  TITLE OF INVENTION: Recombinant Antibodies, and Compositions
;  TITLE OF INVENTION:  and Methods for Making Them
;  FILE REFERENCE: 8321-110
;  CURRENT APPLICATION NUMBER: US/10/225,108A
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: US 09/848,832
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/204,518
;  PRIOR FILING DATE: 2001-05-16
;  PRIOR APPLICATION NUMBER: US 60/314,023
;  PRIOR FILING DATE: 2001-08-21
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-225-108A-4

  Query Match             66.2%;  Score 749.5;  DB 14;  Length 234;
  Best Local Similarity   71.8%;  Pred. No. 1.7e-55;
  Matches  155;  Conservative   13;  Mismatches   43;  Indels    5;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  || ||:|    | | |  | |:||      ||  |:||| |:|
Db         23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |:|:  : || | |:|   ::  | || |||:    ||||||||||
Db         80 ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF 138

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 8
US-10-461-148-2
; Sequence 2, Application US/10461148
; Publication No. US20040013672A1
; GENERAL INFORMATION:
;  APPLICANT: Dietzschold, Bernhard
;  APPLICANT:  Hooper, Douglas C.
;  TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
;  TITLE OF INVENTION:  AND METHODS FOR MAKING AND USING THE SAME
;  FILE REFERENCE: 8321-110CI1-185685
;  CURRENT APPLICATION NUMBER: US/10/461,148
;  CURRENT FILING DATE:  2003-06-13
;  PRIOR APPLICATION NUMBER: US 10/225,108
;  PRIOR FILING DATE: 2002-08-21
;  PRIOR APPLICATION NUMBER: US 60/314,023
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 09/848,832
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/204,518
;  PRIOR FILING DATE: 2000-05-16
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Human
US-10-461-148-2

  Query Match             66.2%;  Score 749.5;  DB 15;  Length 234;
  Best Local Similarity   71.8%;  Pred. No. 1.7e-55;
  Matches  155;  Conservative   13;  Mismatches   43;  Indels    5;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  || ||:|    | | |  | |:||      ||  |:||| |:|
Db         23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |:|:  : || | |:|   ::  | || |||:    ||||||||||
Db         80 ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF 138

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 9
US-10-150-475A-8
; Sequence 8, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, G. et al.
;  TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1211
;  CURRENT APPLICATION NUMBER: US/10/150,475A
;  CURRENT FILING DATE:  2002-05-17
;  PRIOR APPLICATION NUMBER: US 60/307,451
;  PRIOR FILING DATE: 2001-07-24
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Humanised
;   OTHER INFORMATION: Murine Antibody BIWA 8 Light Chain SEQ ID NO: 8
US-10-150-475A-8

  Query Match             66.2%;  Score 749;  DB 14;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 1.7e-55;
  Matches  156;  Conservative   14;  Mismatches   40;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:| :|    :: ||  |:|:||      ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWLQQKPGQAPRILIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  | |    ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213


RESULT 10
US-10-704-522-8
; Sequence 8, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, Gunther
;  APPLICANT:  Baumann, Michael
;  APPLICANT:  Heider, Karl-Heinz
;  TITLE OF INVENTION: Compositions and methods for treating cancer using
;  TITLE OF INVENTION:  cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1414
;  CURRENT APPLICATION NUMBER: US/10/704,522
;  CURRENT FILING DATE:  2003-11-07
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;  PRIOR APPLICATION NUMBER: US 60/429,516
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: EP 02024881
;  PRIOR FILING DATE: 2002-11-08
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;    LENGTH: 213
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Humanised Murine Antibody BIWA 8 Light Chain
US-10-704-522-8

  Query Match             66.2%;  Score 749;  DB 16;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 1.7e-55;
  Matches  156;  Conservative   14;  Mismatches   40;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:| :|    :: ||  |:|:||       ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWLQQKPGQAPRILIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  | |    ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213


RESULT 11
US-10-645-215-8
; Sequence 8, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, Guenther
;  APPLICANT:  Baum, Anke
;  APPLICANT:  Heider, Karl-Heinz
;  TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
;  TITLE OF INVENTION:  Cytotoxic CD44 Antibody Immunoconjugates and
;  TITLE OF INVENTION:  Chemotherapeutic Agents
;  FILE REFERENCE: 1/1383
;  CURRENT APPLICATION NUMBER: US/10/645,215
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: EP 02 018 686.2
;  PRIOR FILING DATE: August 21, 2002
;  PRIOR APPLICATION NUMBER: US 60/405,956
;  PRIOR FILING DATE: August 26, 2002
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;    LENGTH: 213
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Humanised Antibody BIWA 8 Light Chain
US-10-645-215-8

  Query Match             66.2%;  Score 749;  DB 16;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 1.7e-55;
  Matches  156;  Conservative   14;  Mismatches   40;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:| :|    :: ||  |:|:||       ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWLQQKPGQAPRILIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  | |    ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213


RESULT 12
US-10-150-475A-4
; Sequence 4, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, G. et al.
;  TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1211
;  CURRENT APPLICATION NUMBER: US/10/150,475A
;  CURRENT FILING DATE:  2002-05-17
;  PRIOR APPLICATION NUMBER: US 60/307,451
;  PRIOR FILING DATE: 2001-07-24
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;    LENGTH: 213
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Humanised
;    OTHER INFORMATION: Murine Antibody BIWA 4 Light Chain SEQ ID NO: 4
US-10-150-475A-4

  Query Match             66.0%;  Score 747;  DB 14;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 2.4e-55;
  Matches  156;  Conservative   13;  Mismatches   41;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:| :|    :: ||  | |:||       ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWYQQKPGQAPRLLIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  | |    ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213


RESULT 13
US-10-704-522-4
; Sequence 4, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, Gunther
;  APPLICANT:  Baumann, Michael
;  APPLICANT:  Heider, Karl-Heinz
;  TITLE OF INVENTION: Compositions and methods for treating cancer using
;  TITLE OF INVENTION:  cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1414
;  CURRENT APPLICATION NUMBER: US/10/704,522
;  CURRENT FILING DATE:  2003-11-07
;  PRIOR APPLICATION NUMBER: US 60/429,516
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: EP 02024881
;  PRIOR FILING DATE: 2002-11-08
;  NUMBER OF SEQ ID NOS: 9
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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-10-704-522-4

  Query Match             66.0%;  Score 747;  DB 16;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 2.4e-55;
  Matches  156;  Conservative   13;  Mismatches   41;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:| :|    :: ||  | |:||      ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWYQQKPGQAPRLLIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  | |    ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213


RESULT 14
US-10-645-215-4
; Sequence 4, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, Guenther
;  APPLICANT:  Baum, Anke
;  APPLICANT:  Heider, Karl-Heinz
;  TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
;  TITLE OF INVENTION:  Cytotoxic CD44 Antibody Immunoconjugates and
;  TITLE OF INVENTION:  Chemotherapeutic Agents
;  FILE REFERENCE: 1/1383
;  CURRENT APPLICATION NUMBER: US/10/645,215
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: EP 02 018 686.2
;  PRIOR FILING DATE: August 21, 2002
;  PRIOR APPLICATION NUMBER: US 60/405,956
;  PRIOR FILING DATE: August 26, 2002
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-10-645-215-4

  Query Match             66.0%;  Score 747;  DB 16;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 2.4e-55;
  Matches  156;  Conservative   13;  Mismatches   41;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:| :|    :: ||  | |:||      ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWYQQKPGQAPRLLIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  | |    ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213


RESULT 15
US-10-307-724-122
; Sequence 122, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Frederickson, Shana
;  APPLICANT:  Renshaw, Mark
;  TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
;  FILE REFERENCE: 1087-2cip
;  CURRENT APPLICATION NUMBER: US/10/307,724
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: US 60/251,448
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/288,889
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/294,068
;  PRIOR FILING DATE: 2001-05-29
;  PRIOR APPLICATION NUMBER: US 10/006,593
;  PRIOR FILING DATE: 2001-12-05
;  NUMBER OF SEQ ID NOS: 134
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: antibody light chain
US-10-307-724-122

  Query Match             65.5%;  Score 742;  DB 15;  Length 215;
  Best Local Similarity   70.8%;  Pred. No. 6.6e-55;
  Matches  153;  Conservative   16;  Mismatches   43;  Indels    4;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||  ||:||:|     :|:|  | |:||      || | ::|| |:|
Db          3 VLTQSPGTLSLSPGERATLSCRAS--QSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              |||||  |    |||:  : || | |:|  : |  | || |||: :  ||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEI-KRTVAAPSVFIF 119

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||| ||||||||||
Db        180 LTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 215


Search completed: June  7, 2005, 16:18:38
Job time : 102 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:39:10 ; Search time 25 Seconds
(without alignments)
839.010 Million cell updates/sec

Title: US-09-671-953B-5
Perfect score: 1132
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	740	65.4	215	2	JE0242	Ig kappa chain NIG
2	729	64.4	215	2	JE0244	Ig kappa chain NIG
3	724.5	64.0	214	2	PC4156	Ig lambda chain V
4	716	63.3	215	2	JE0243	Ig kappa chain NIG
5	682.5	60.3	216	2	JE0241	Ig kappa chain Am3
6	675	59.6	215	2	A23746	Ig kappa chain V-I
7	578.5	51.1	135	2	S52059	JC-kappa protein -
8	552.5	48.8	240	2	S06084	Ig kappa chain pre
9	544	48.1	106	1	K3HU	Ig kappa chain C r
10	543.5	48.0	287	4	PC4402	pelB leader/Ig hea
11	537	47.4	128	2	S52450	Ig lambda chain V
12	530.5	46.9	220	2	A31790	Ig kappa chain V r
13	529	46.7	129	1	L1MS4E	Ig lambda-1 chain
14	522	46.1	235	2	S25058	Ig kappa chain - m
15	521	46.0	113	2	S06819	Ig lambda chain V
16	519.5	45.9	112	2	S06818	Ig lambda chain V
17	517	45.7	106	2	S20654	Ig lambda chain V
18	515	45.5	219	2	S38865	Ig kappa chain - m
19	514	45.4	225	2	S37484	Ig kappa chain - m
20	509.5	45.0	114	2	S06820	Ig lambda chain V
21	509.5	45.0	234	2	S14237	Ig kappa chain pre
22	509	45.0	99	2	A37927	Ig kappa chain C r
23	506.5	44.7	230	2	S33161	Ig kappa chain - s
24	503.5	44.5	218	2	S68241	Ig kappa chain V r
25	503	44.4	99	2	S26653	Ig kappa chain C r
26	501.5	44.3	214	2	S68212	Ig kappa chain (Ma
27	499.5	44.1	225	2	JL0029	Ig kappa chain pre
28	498.5	44.0	218	2	JC5810	monoclonal antibod
29	497.5	43.9	234	2	S01320	Ig kappa chain pre
30	495.5	43.8	114	2	S06822	Ig lambda chain V
31	495	43.7	113	2	B54256	Ig lambda-1 chain
32	492	43.5	217	2	S42772	Ig kappa chain - m
33	492	43.5	219	2	S16112	Ig kappa chain V r
34	491	43.4	129	1	L2MS35	Ig lambda-2 chain
35	488.5	43.2	219	2	PC4203	Ig kappa chain (mo
36	485	42.8	235	2	S25749	Ig lambda chain -
37	484.5	42.8	99	2	PH1089	Ig lambda chain V
38	482	42.6	99	2	S14582	Ig lambda chain V
39	482	42.6	113	2	S06821	Ig lambda chain V
40	482	42.6	219	2	S52028	Ig kappa chain - m
41	477	42.1	97	2	PH1090	Ig lambda chain V
42	477	42.1	116	1	L1MSV	Ig lambda-1 chain
43	475.5	42.0	210	2	A56169	Ig kappa chain V r
44	472	41.7	99	2	S14584	Ig lambda chain V
45	469	41.4	100	2	PH1088	Ig lambda chain V

ALIGNMENTS

RESULT 1
JE0242
Ig kappa chain NIG26 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda,
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mu
A;Reference number: JE0241
A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 740; DB 2; Length 215;
Best Local Similarity 70.4%; Pred. No. 7.9e-49;
Matches 152; Conservative 17; Mismatches 43; Indels 4; Gaps 3;

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Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
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Db          3 VLTQSPGTLSLSPGERATLSCRAS--QSVSNNYLAWYQQKPGQAPSLLIYDASSRATGIP 60

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              |||||  |    |||:| : || | |:|  :    | || |||: :  ||||||||||
Db         61 DRFSGSGSGTDFILTISGLEPEDFAVYYCQQYDRPPWTFGQGTKVEI-KRTVAAPSVFIF 119

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
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RESULT 2
JE0244
Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL am
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

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  Query Match             64.4%;  Score 729;  DB 2;  Length 215;
  Best Local Similarity   71.2%;  Pred. No. 5.4e-48;
  Matches  156;  Conservative   14;  Mismatches   39;  Indels   10;  Gaps    6;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: |||| ||:||:|      || | | |:||      ||   : || |:|
Db          3 VLTQSPATLSVSPGERATLSCRAS--QSVHSNLA-WYQQKPGQAPRLLIYRASTRATGIP 59

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLW---VFGGGTKLTVLSRTVAAPSV 119
              |||||| |    |||:  |:|| | |:|  : :  |    ||||||: :  ||||||||
Db         60 ARFSGSGSGTDFILTISSLQSEDFALYYCQQYNT--WPPLTFGGGTKVEI-KRTVAAPSV 116

Qy        120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176

Qy        180 SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||| ||||||||||
Db        177 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215


RESULT 3
PC4156
Ig lambda chain V region MabB23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C;Accession: PC4156
R;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 169, 237-239, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mc
A;Reference number: PC4155; MUID:96194809; PMID:8647454
A;Accession: PC4156
A;Molecule type: mRNA
A;Residues: 1-214 <KWA>
A;Cross-references: GB:U28967; NID:g1262178; PIDN:AAC52488.1; PID:g1262179
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-214/Product: light chain #status predicted <MAT>
F;98-110/Region: V region
F;130-198/Domain: immunoglobulin homology <IMM>

  Query Match             64.0%;  Score 724.5;  DB 2;  Length 214;
  Best Local Similarity   66.5%;  Pred. No. 1.2e-47;
  Matches  145;  Conservative   23;  Mismatches   43;  Indels    7;  Gaps    3;

Qy          3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |||||||||||||||||||||: |||||||||:||||||||||||||||| ||||
Db          2 AVVTQESALTTSPGETVTLTCRSNTGAVTTSNYASWVQEKPDHLFTGLIGGTNNRVPGVP 61

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              |||||||||||||||||||||||| |||||| |  |||||||||||| :  ::||| :|
Db         62 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWNSNHWVFGGGTKLTVLGQPKSSPSVTLF 121

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST--YSLS 180
              ||| |:|::  |::|| : :|||     | ||||    :  :|   | | || |   | |
Db        122 PPSSEELETNKATLVCTITDFYPGVVTVDWKVDG---TPVTQGMETTQPSKQSNNKYMAS 178

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              | |||:   :|:|  |:|:|||:|     | || :| :|
Db        179 SYLTLTARAWERHSSYSCQVTHEG--HTVEKSLSRADC 214


RESULT 4
JE0243
Ig kappa chain NIG93 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0243
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0243
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             63.3%;  Score 716;  DB 2;  Length 215;
  Best Local Similarity   69.7%;  Pred. No. 5.1e-47;
  Matches  152;  Conservative   13;  Mismatches   45;  Indels    8;  Gaps    4;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:||:|     |      |  :|       ||   : || |||
Db          3 VMTQSPATLSVSPGERATLSCRASQSVATN---VVWYMQKLGQAPRLLIYDASTRATGVP 59

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLW--VFGGGTKLTVLSRTVAAPSVF 120
              ||||||  | :  |||:  |:|| | |:|   ::  |   || |||:    |||||||||
Db         60 ARFSGSGSGTEFTLTISSLQSEDFAIYYCQ--HNNAWPPTFGQGTKVETKRRTVAAPSVF 117

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 177

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||| ||||||||||
Db        178 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215


RESULT 5
JE0241
Ig kappa chain Am37 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0241
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0241
A;Molecule type: protein
A;Residues: 1-216 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>

  Query Match             60.3%;  Score 682.5;  DB 2;  Length 216;
  Best Local Similarity   66.8%;  Pred. No. 1.7e-44;
  Matches  145;  Conservative   14;  Mismatches   53;  Indels    5;  Gaps    4;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTS-NYANWVQEKPDHLFTGLIGGTNNRAPGV 61
              |:||    |  | ||  |: |:||   :  | |:  | |:||      |:   | |  ||
Db          3 VLTQSPDFLAVSLGERATINCKSSQSVLYNSKNFLAWYQQKPGQ--PKLLIWANVRESGV 60

Qy         62 PARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFI 121
              | || || :|    |||:  | |  | |:|  :||  : || | :| :  ||||||||||
Db         61 PDRFRGSGVGTDFTLTISNLQAELVAVYYCQQYYSTPYSFGQGGRLEI-KRTVAAPSVFI 119

Qy        122 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 179

Qy        182 TLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |   |||||||||||||||||||| ||||||||||
Db        180 TTLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216


RESULT 6
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91131575; PMID:1993660
```

A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 <LEO>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 59.6%; Score 675; DB 2; Length 215;
Best Local Similarity 68.8%; Pred. No. 6.3e-44;
Matches 148; Conservative 15; Mismatches 48; Indels 4; Gaps 3;

```
Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:  :|     :|||  | |:||       ||   ::|| |:|
Db          3 VLTQSPATLSLSPGERATLSGGAS--QSVSSNYLAWYQQKPGQAPRLLIYDASSRATGIP 60

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
               |||||  |    |||:  : || | |:   : |    ||||||: :  ||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYGQQYGSSPLTFGGGTKVEI-KRTVAAPSVFIF 119

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVGLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGE 217
              ||||||||||||||| |||||||| |||||||||
Db        180 LTLSKADYEKHKVYAGEVTHQGLSSPVTKSFNRGE 214
```

RESULT 7
S52059
JC-kappa protein - human
C;Species: Homo sapiens (man)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
C;Accession: S52059
R;Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S.;
EMBO J. 13, 5937-5943, 1994
A;Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy c
A;Reference number: S52059; MUID:95112804; PMID:7813432
A;Accession: S52059
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <FRA>
C;Superfamily: pre-B cell omega light chain; immunoglobulin homology

Query Match 51.1%; Score 578.5; DB 2; Length 135;
Best Local Similarity 89.7%; Pred. No. 7.2e-37;
Matches 113; Conservative 3; Mismatches 5; Indels 5; Gaps 2;

```
Qy         93 LWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW 152
              ||    | || |||: :  ||||||||||||||||||||||||||||||||||||||||
Db         15 LW----WTFGQGTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW 69

Qy        153 KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKS 212
              ||||||||||||||||||||||||||||||||||||||:|||||||||| |||||
Db         70 KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKLYACEVTHQGLSSPVTKS 129

Qy        213 FNRGEC 218
              ||||||
Db        130 FNRGEC 135
```

RESULT 8
S06084
Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A;Reference number: S06084; MUID:90016888; PMID:2508067
A;Accession: S06084
A;Molecule type: mRNA
A;Residues: 1-240 <CRO>
A;Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-240/Product: Ig kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 48.8%; Score 552.5; DB 2; Length 240;
Best Local Similarity 53.4%; Pred. No. 1.2e-34;
Matches 117; Conservative 24; Mismatches 73; Indels 5; Gaps 3;

```
Qy          4 VVTQE-SALTTSPGETVTLTCRSS---IGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAP 59
              |:||  |:|  | |||||: |:||     :    ||  | |:||       ||   : |
Db         23 VMTQSPSSLAVSAGETVTINCKSSQSLFYSGNQKNYLAWYQQKPGQSPKLLIYWASTRQS 82

Qy         60 GVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSV 119
              ||| || ||  |    |||:  | || | |:|  :|   : || ||||  | |  |||:|
Db         83 GVPDRFIGSGSGTDFTLTISSVQAEDLAIYYCLQYYETPYTFGAGTKLE-LKRADAAPTV 141

Qy        120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
               |||||  ||| :| |||||||:||||||:  |:||:|   :     :|||:|||||||||:
Db        142 SIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGVLDSVTDQDSKDSTYSM 201

Qy        180 SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||:|||||| | :| ||| |:  | || |||||  ||
Db        202 SSTLSLSKADYESHNLYTCEVVHKTSSSPVVKSFNRNEC 240
```

RESULT 9
K3HU
Ig kappa chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02
R;Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.
Biochemistry 9, 3155-3161, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequenc
A;Reference number: A90562; MUID:71064023; PMID:5489770
A;Contents: myeloma protein Eu
A;Accession: B90562
A;Molecule type: protein
A;Residues: 1-106 <GOT>
A;Cross-references: UNIPROT:P01834
A;Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfi
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; Eu, disulfide bonds
R;Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
A;Reference number: A91651; MUID:72188439; PMID:5027703
A;Contents: Bence Jones protein Ti
A;Accession: A91651
A;Molecule type: protein
A;Residues: 1-106 <SUT>
R;Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
Cell 22, 197-207, 1980
A;Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conser
A;Reference number: A90806; MUID:81042304; PMID:6775818
A;Accession: A90806
A;Molecule type: DNA
A;Residues: 1-106 <HIE>
A;Cross-references: GB:J00241; NID:g33140; PIDN:CAA23823.1; PID:g1335148
A;Note: the sequence was determined from the germline gene
R;Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne,
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,
A;Reference number: A94417
A;Contents: Bence Jones protein Roy
A;Accession: A94417

```
A;Molecule type: protein
A;Residues: 1-44,'A',46-56,'Q',58-82,'L',84-106 <HIL>
A;Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu
R;Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
A;Title: Die volstaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).
A;Reference number: A91639; MUID:68242259; PMID:5586923
A;Contents: Bence Jones protein Cum
A;Accession: A91639
A;Molecule type: protein
A;Residues: 1-56,'Q',58-106 <HI2>
R;Titani, K.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 244, 3550-3560, 1969
A;Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete
A;Reference number: A92047; MUID:69234734; PMID:4893682
A;Contents: Bence Jones protein Ag
A;Accession: A92047
A;Molecule type: protein
A;Residues: 1-13,'N',15-106 <TIT>
R;Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
Science 169, 56-59, 1970
A;Title: Macroglobulin structure: variable sequence of light and heavy chains.
A;Reference number: A94242; MUID:70201507; PMID:5447531
A;Contents: Waldenstrom's macroglobulin Ou
A;Accession: A94242
A;Molecule type: protein
A;Residues: 1-13,'N',15-106 <KOH>
R;Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
Am. J. Hum. Genet. 48, 613-620, 1991
A;Title: Km typing with PCR: application to population screening.
A;Reference number: A37927; MUID:91150772; PMID:1900145
A;Accession: B37927
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 8-106 <KUR>
A;Note: allotype Inv(3)
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Genetics:
A;Gene: GDB:IGKC
A;Cross-references: GDB:120088; OMIM:147200
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-88/Domain: immunoglobulin homology <IMM>
F;26-86/Disulfide bonds: #status experimental
F;106/Disulfide bonds: interchain (to heavy chain) #status experimental

  Query Match             48.1%;  Score 544;  DB 1;  Length 106;
  Best Local Similarity   99.1%;  Pred. No. 2.2e-34;
  Matches  105;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        113 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

Qy        173 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||||||||||||||| ||||||||||
Db         61 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106


RESULT 10
PC4402
pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
C;Species: synthetic
C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C;Accession: PC4402
R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem. 122, 322-329, 1997
A;Title: Construction, bacterial expression, and characterization of hapten-specific sin
A;Reference number: PC4402
A;Accession: PC4402
A;Molecule type: DNA
A;Residues: 1-287 <SUZ>
C;Keywords: fusion protein

  Query Match             48.0%;  Score 543.5;  DB 4;  Length 287;
  Best Local Similarity   53.4%;  Pred. No. 6.9e-34;
  Matches  126;  Conservative   14;  Mismatches   49;  Indels   47;  Gaps    6;

Qy          3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         27 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 86

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAP----- 117
              |||||||||||||||||||||||| ||||||||  ||||||||||||||     |
Db         87 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLSSADDAKKDDAK 146

Qy        118 -------------SVFIFPPSDEQLKSG-TASVVCLLNNFYPREAKVQW----------- 152
                          | :  |  | :| | :  : |  : :      : |
Db        147 KDDAKKDDAKKDGQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEW 206

Qy        153 --KVDNALQSG--------NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC 198
                ::|    ||         |: ::|       : |   |:||      |   || |
Db        207 IGRIDP--NSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLT-----SEDSAVYYC 255


RESULT 11
S52450
Ig lambda chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52450
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged gen
A;Reference number: S52445
A;Accession: S52450
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 <BER>
A;Cross-references: EMBL:X82687; NID:g673448; PIDN:CAA58008.1; PID:g673449
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-111/Domain: immunoglobulin homology <IMM>

  Query Match             47.4%;  Score 537;  DB 2;  Length 128;
  Best Local Similarity   96.3%;  Pred. No. 9.1e-34;
  Matches  104;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         21 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVL 110
              |||||||||||||||||||||||| ||||||||  ||||||||||||
Db         81 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 128


RESULT 12
A31790
Ig kappa chain V region (17/9) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: A31790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data for an an
A;Reference number: A92686; MUID:89034213; PMID:3182835
```

A;Accession: A31790
A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 530.5; DB 2; Length 220;
Best Local Similarity 51.6%; Pred. No. 5e-33;
Matches 113; Conservative 26; Mismatches 75; Indels 5; Gaps 3;

```
Qy          4 VVTQE-SALTTSPGETVTLTCRSS---IGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAP 59
              |:||  |:|| : || ||::| ||     :    ||  | |:||       ||   : |
Db          3 VMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQQKPGQPPKVLIYWASTRES 62

Qy         60 GVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSV 119
              ||| ||:||  |    |||:  | || | |:|   ||    |||||||  | |  |||:|
Db         63 GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSNPLTFGGGTKLE-LKRADAAPTV 121

Qy        120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
               ||||| ||| || ||||| ||||||::  |:||:| : :       | |:||||||||:
Db        122 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 181

Qy        180 SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||:| :||:|  | || ||:  : |: |||||  ||
Db        182 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 220
```

RESULT 13
L1MS4E
Ig lambda-1 chain precursor V regions (MOPC 104E, RPC20, J558, S104, S178, H2020, S43)
C;Species: Mus musculus (house mouse)
C;Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004
C;Accession: B93815; B93775; C93775; A93784; B93784; C93784; A90780; C93282; A01995
R;Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A;Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors
A;Reference number: A93815; MUID:77148916; PMID:403522
A;Contents: MOPC 104E
A;Accession: B93815
A;Molecule type: protein
A;Residues: 1-29 <BUR>
A;Cross-references: UNIPROT:P01724
A;Note: this precursor was synthesized in a cell-free system directed by messenger RNA i
d after synthesis
R;Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
A;Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
A;Reference number: A93775; MUID:71107854; PMID:5276767
A;Contents: MOPC 104E; RPC 20
A;Accession: B93775
A;Molecule type: protein
A;Residues: 'Z',21-25,'Q',27-129 <APP>
A;Accession: C93775
A;Molecule type: protein
A;Residues: 20-129 <AP2>
A;Note: compositions and partial sequences of RPC 20 show no differences from MOPC 104E
R;Cesari, I.M.; Weigert, M.
Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
A;Title: Mouse lambda-chain sequences.
A;Reference number: A93784; MUID:73229669; PMID:4516208
A;Contents: J558; S104; S178
A;Accession: A93784
A;Molecule type: protein
A;Residues: 20-129 <CES>
A;Accession: B93784
A;Molecule type: protein
A;Residues: 20-129 <CE2>
A;Accession: C93784
A;Molecule type: protein
A;Residues: 20-43,'N',45-70,'N',72-115,'R',117-129 <CE3>
A;Note: these proteins were isolated from serum or urine of tumor-bearing mice

R;Bernard, O.; Hozumi, N.; Tonegawa, S.
Cell 15, 1133-1144, 1978
A;Title: Sequences of mouse immunoglobulin light chain genes before and after somatic ch
A;Reference number: A90780; MUID:79084170; PMID:103630
A;Contents: H2020
A;Accession: A90780
A;Molecule type: DNA
A;Residues: 1-43,'T',45-50,'G',52-58,'E',60-89,'D',91-129 <BER>
A;Note: the sequence was determined from the differentiated gene
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D
Nature 298, 380-382, 1982
A;Title: Somatic variants of murine immunoglobulin lambda light chains.
A;Reference number: A93282; MUID:82220143; PMID:6283385
A;Contents: S43
A;Accession: C93282
A;Molecule type: DNA
A;Residues: 1-58,'E',60-89,'D',91-98,'T',100-105,'M',107-129 <BOT>
A;Note: the sequence was determined from the differentiated gene
C;Comment: The MOPC 104E sequence is shown.
C;Genetics:
A;Introns: 16/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; pyroglutamic acid
F;1-19/Domain: signal sequence #status experimental <SIG>
F;20-129/Domain: Ig lambda-1 chain precursor V region #status experimental <MAT>
F;34-111/Domain: immunoglobulin homology <IMM>
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime
F;41-109/Disulfide bonds: #status predicted

Query Match 46.7%; Score 529; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 3.7e-33;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |||||||||||||||||||||||| ||||||||||||:||||||||||||||||||||
Db         21 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQQKPDHLFTGLIGGTNNRAPGVP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVL 110
              |||||||||:|||||||||||||||| ||||||||  ||||||||||
Db         81 ARFSGSLIGNKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 128
```

RESULT 14
S25058
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: S25058
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
A;Reference number: S25057
A;Accession: S25058
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-235 <FIS>
A;Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-111/Domain: immunoglobulin homology <IMM>

Query Match 46.1%; Score 522; DB 2; Length 235;
Best Local Similarity 50.5%; Pred. No. 2.3e-32;
Matches 109; Conservative 29; Mismatches 72; Indels 6; Gaps 3;

```
Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | :: |||| ||:|| :|    :: :   | |:|        |  |:  | |||
Db         25 VLTQSPAIMSASPGEKVTMTCSAS----SSVSKMQWYQQKSGTSPKRWIYDTSKLASGVP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              |||||  |   :|||:  : || | |:|  | |    || ||||  | |  |||:| ||
Db         81 GRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE-LKRADAAPTVSIF 139
```

```
Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||| ||| || ||||| |||||||::  |:||:| : :      | |:||||||||:|||
Db        140 PPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||:| :||:|  | || ||:  : |: ||||| ||
Db        200 LTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 235


RESULT 15
S06819
Ig lambda chain V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C;Accession: S06819
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06819
A;Molecule type: mRNA
A;Residues: 1-113 <MIL>
A;Cross-references: EMBL:X17168; NID:g52251; PIDN:CAA35046.1; PID:g930172
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-91/Domain: immunoglobulin homology <IMM>
F;21-89/Disulfide bonds: #status predicted

  Query Match             46.0%;  Score 521;  DB 2;  Length 113;
  Best Local Similarity   94.4%;  Pred. No. 1.3e-32;
  Matches  102;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 60

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVL 110
              |||||||||||||||||||||||| |||:||||   ||||||||||
Db         61 ARFSGSLIGDKAALTITGAQTEDEAIYFCSLWYSNHLVFGGGTKLTVL 108


Search completed: June  7, 2005, 16:01:07
Job time : 26 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:37:31 ; Search time 111 Seconds
(without alignments)
1005.705 Million cell updates/sec

Title: US-09-671-953B-5
Perfect score: 1132
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	734	64.8	235	2	Q6PJF2	Q6pjf2 homo sapien
2	733	64.8	235	2	Q6GMW0	Q6gmw0 homo sapien
3	732	64.7	236	2	Q6GMW1	Q6gmw1 homo sapien
4	727.5	64.3	236	2	Q7Z3Y4	Q7z3y4 homo sapien
5	727	64.2	234	2	Q7Z473	Q7z473 homo sapien
6	723.5	63.9	236	2	Q6PIH7	Q6pih7 homo sapien
7	722.5	63.8	236	2	Q6GMX9	Q6gmx9 homo sapien
8	721.5	63.7	236	2	Q6P5S8	Q6p5s8 homo sapien
9	721	63.7	235	2	Q6GMV9	Q6gmv9 homo sapien
10	720.5	63.6	236	2	Q6GMX0	Q6gmx0 homo sapien
11	717.5	63.4	236	2	Q6PIL8	Q6pil8 homo sapien
12	715.5	63.2	236	2	Q6GMX8	Q6gmx8 homo sapien
13	704	62.2	236	2	Q6PIT5	Q6pit5 homo sapien
14	702.5	62.1	236	2	Q6PIH4	Q6pih4 homo sapien
15	697	61.6	239	2	Q8TCD0	Q8tcd0 homo sapien
16	696	61.5	240	2	Q6PIH6	Q6pih6 homo sapien
17	694	61.3	239	2	Q8NEK0	Q8nek0 homo sapien
18	666	58.8	239	2	Q6P491	Q6p491 homo sapien
19	564.5	49.9	120	2	Q6P5R5	Q6p5r5 homo sapien
20	544	48.1	106	1	KAC_HUMAN	P01834 homo sapien
21	535	47.3	129	1	LV1E_MOUSE	P01727 mus musculu
22	530	46.8	129	1	LV1D_MOUSE	P01726 mus musculu
23	529	46.7	129	1	LV1B_MOUSE	P01724 mus musculu
24	523	46.2	129	2	Q8VDE2	Q8vde2 mus musculu
25	522.5	46.2	238	2	Q66JS7	Q66js7 mus musculu
26	521	46.0	110	1	LV1C_MOUSE	P01725 mus musculu
27	514.5	45.5	113	2	Q8CGS1	Q8cgs1 mus musculu
28	510.5	45.1	236	2	Q7TS98	Q7ts98 mus musculu
29	507.5	44.8	109	2	Q9ET13	Q9et13 mus musculu
30	502	44.3	219	2	Q65ZC0	Q65zc0 mus musculu
31	497.5	43.9	241	2	Q63ZX4	Q63zx4 mus musculu
32	491	43.4	129	1	LV2B_MOUSE	P01729 mus musculu
33	477	42.1	117	1	LV1A_MOUSE	P01723 mus musculu
34	454	40.1	117	1	LV2A_MOUSE	P01728 mus musculu
35	442.5	39.1	236	2	Q8NEJ1	Q8nej1 homo sapien
36	440	38.9	235	2	Q6IN99	Q6in99 homo sapien
37	435	38.4	248	2	Q7SYU1	Q7syu1 xenopus lae
38	432	38.2	233	2	Q8TBC9	Q8tbc9 homo sapien
39	430.5	38.0	230	2	Q7Z2U3	Q7z2u3 homo sapien
40	430.5	38.0	236	2	Q6PIQ7	Q6piq7 homo sapien
41	428.5	37.9	236	2	Q6GMV7	Q6gmv7 homo sapien
42	428.5	37.9	236	2	Q6IPQ0	Q6ipq0 homo sapien
43	427.5	37.8	234	2	Q7Z2U7	Q7z2u7 homo sapien
44	426.5	37.7	236	2	Q6GMX4	Q6gmx4 homo sapien
45	426	37.6	231	2	Q6GNB8	Q6gnb8 xenopus lae

ALIGNMENTS

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RESULT 1
Q6PJF2
ID   Q6PJF2      PRELIMINARY;      PRT;   235 AA.
AC   Q6PJF2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016380; AAH16380.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25520 MW;  F33A145A396BA285 CRC64;

  Query Match             64.8%;  Score 734;  DB 2;  Length 235;
  Best Local Similarity   70.4%;  Pred. No. 1.5e-56;
  Matches  152;  Conservative   18;  Mismatches   42;  Indels    4;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:|| | |: |||| ||:||:|   : :| |  | |:||      |: |:::|| |:|
Db         23 VLTQSPATLSLSPGERATLSCRAS--QIVSSAYLAWYQQKPGQAPRLLMFGSSSRATGIP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              |||||  |    |||:  : || | |:|  : |    || |||: :  ||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSQGTFGPGTKVDI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 2
Q6GMW0
ID   Q6GMW0      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMW0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073792; AAH73792.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25765 MW;  4360C36B6D4133F5 CRC64;

  Query Match             64.8%;  Score 733;  DB 2;  Length 235;
  Best Local Similarity   70.5%;  Pred. No. 1.9e-56;
  Matches  153;  Conservative   17;  Mismatches   41;  Indels    6;  Gaps    4;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:|| | |: |||| ||:||:|    : ||   | |::|      || | ::|  |:|
Db         23 VMTQSPATLSVSPGERATLSCRAS---QSISNNLAWYQQRPGQAPRLLIYGASSRVTGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYS-CLWVFGGGTKLTVLSRTVAAPSVFI 121
              |||||  | :  |:|:  |:|| | |||  :    |: || |||| :  ||||||||||
Db         80 GRFSGSGSGTEFTLSISSLQSEDFAVYFCQQYNDWLLYTFGQGTKLEI-KRTVAAPSVFI 138

Qy        122 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 198

Qy        182 TLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        199 TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 3
Q6GMW1
ID   Q6GMW1      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMW1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073791; AAH73791.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
```

```
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25751 MW;  5BFE6A087AFAC437 CRC64;

  Query Match             64.7%;  Score 732;  DB 2;  Length 236;
  Best Local Similarity   70.0%;  Pred. No. 2.3e-56;
  Matches  154;  Conservative   16;  Mismatches   44;  Indels    6;  Gaps    4;

Qy          1 RSAV-VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              | |: :||  |:|: | |: ||:|||:| |    ||   | |:||      ||   ::
Db         21 RCAIQMTQSPSSLSASVGDRVTITCRASQG---ISNDLGWYQQKPGKAPKLLIYAASSLQ 77

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS 118
               |||:|||||  |    |||:  | || | |:|   |:  | || |||: :  |||||||
Db         78 SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYPWTFGQGTKVEI-KRTVAAPS 136

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 196

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||| ||||||||||
Db        197 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 4
Q7Z3Y4
ID   Q7Z3Y4      PRELIMINARY;      PRT;   236 AA.
AC   Q7Z3Y4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005332; AAH05332.1; -.
DR   HSSP; P01834; 1HEZ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25702 MW;  7FBFE4ED23084BC6 CRC64;

  Query Match             64.3%;  Score 727.5;  DB 2;  Length 236;
  Best Local Similarity   70.7%;  Pred. No. 5.7e-56;
  Matches  152;  Conservative   15;  Mismatches   43;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  |:|: | |:|||:|||:|      |||  | |:||      || | ::   || :
Db         26 MTQSPSSLSASVGDTVTITCRAS---QDISNYLAWFQQKPGKAPKSLIYGASSLQSGVQS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              :|||| |    |||:  | || | |:|  : |    || |||| :  ||||||||||||
Db         83 KFSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEI-KRTVAAPSVFIFP 141

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 5
Q7Z473
ID   Q7Z473      PRELIMINARY;      PRT;   234 AA.
AC   Q7Z473;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
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RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056256; AAH56256.1; -.
DR   HSSP; P01834; 1HEZ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25674 MW;  1A2C259BAB51BC0F CRC64;

  Query Match             64.2%;  Score 727;  DB 2;  Length 234;
  Best Local Similarity   68.2%;  Pred. No. 6.3e-56;
  Matches  150;  Conservative   20;  Mismatches   44;  Indels    6;  Gaps    4;

Qy          1 RSAV-VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              | |: :||  |: : | |: ||:|||:|    :  :|  | |:||      ||   :
Db         19 RCAIRMTQSPSSFSASTGDRVTITCRAS---QSIGSYLAWYQQKPGKAPQLLIYAASTLQ 75

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS 118
              |||:|||||  |    |:|:  |:|| | |:|  :|:  | || |||: :  |||||||
Db         76 SGVPSRFSGSASGTDFTLSISCLQSEDFATYYCQQYYTYPWTFGQGTKVEI-KRTVAAPS 134

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 194

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||| ||||||||||
Db        195 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 6
Q6PIH7
ID   Q6PIH7      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034141; AAH34141.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25603 MW;  8BC561106861213F CRC64;

  Query Match             63.9%;  Score 723.5;  DB 2;  Length 236;
  Best Local Similarity   70.7%;  Pred. No. 1.3e-55;
  Matches  152;  Conservative   14;  Mismatches   44;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  | |: | |: ||:|||:| |    |:|  | |:||      ||   :   |||:
Db         26 LTQSPSFLSASVGDRVTITCRASQG---ISSYLAWYQQKPGKAPNLLIYAASTLQSGVPS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  | :  |||:  | || | |:|    |    ||||||: :  ||||||||||
Db         83 RFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSSPPTFGGGTKVEI-KRTVAAPSVFIFP 141

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 7
Q6GMX9
ID   Q6GMX9      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073763; AAH73763.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25924 MW;  FDE2093DC560CFF7 CRC64;

  Query Match             63.8%;  Score 722.5;  DB 2;  Length 236;
  Best Local Similarity   69.3%;  Pred. No. 1.6e-55;
  Matches  149;  Conservative   18;  Mismatches   43;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  |:|: | |  ||:|||:|      | :  | |::|:     ||  |::   |||:
Db         26 MTQSPSSLSASVGHRVTITCRAS---QNVSRWLAWYQQRPEKAPKSLIYATSSLHSGVPS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  |    |||:  | || | |:|  : :    ||||||: :  ||||||||||||
Db         83 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNTYPLTFGGGTKVEI-KRTVAAPSVFIFP 141

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 8
Q6P5S8
ID   Q6P5S8      PRELIMINARY;      PRT;   236 AA.
AC   Q6P5S8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062704; AAH62704.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25773 MW;  953E37BEB4FF5F27 CRC64;

  Query Match             63.7%;  Score 721.5;  DB 2;  Length 236;
  Best Local Similarity   70.0%;  Pred. No. 1.9e-55;
  Matches  152;  Conservative   16;  Mismatches   44;  Indels    5;  Gaps    4;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||  ||:||:|      |::  | |::|      || | ::|| |:|
Db         23 VLTQSPGTLSFSPGERATLSCRAS--QTVFSSHLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALW-YSCLWVFGGGTKLTVLSRTVAAPSVFI 121
              |||||  |    ||||  : || | |||  :  |    |||||:: :  ||||||||||
Db         81 DRFSGSGSGTDFTLTITRLEPEDFAVYFCQQYGTSPSLTFGGGTRVEI-KRTVAAPSVFI 139

Qy        122 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 199

Qy        182 TLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        200 TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 9
Q6GMV9
ID   Q6GMV9      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMV9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073793; AAH73793.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25646 MW;  DF32B580BAD19E4B CRC64;

  Query Match             63.7%;  Score 721;  DB 2;  Length 235;
  Best Local Similarity   69.4%;  Pred. No. 2.1e-55;
  Matches  150;  Conservative   15;  Mismatches   47;  Indels    4;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||   |:||:|      | |  | |:||      |:   : || |:|
Db         23 VLTQSPGTLSLSPGERAALSCRAS--QSVNSKYLAWYQQKPGQAPRLLMYAASIRATGIP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
              |||||  |    |||:  ::|| | |||  : :    ||||||: :  ||||||||||
Db         81 DRFSGSGSGTDFTLTISRLESEDFALYFCQQYGTSPLTFGGGTKVEI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 10
Q6GMX0
ID   Q6GMX0      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073775; AAH73775.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25807 MW;  864EA08C7E92BF8F CRC64;

  Query Match             63.6%;  Score 720.5;  DB 2;  Length 236;
  Best Local Similarity   69.3%;  Pred. No. 2.4e-55;
  Matches  149;  Conservative   17;  Mismatches   44;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  |:|: | |: ||:|||:|      :|| || | ||      ||   ::   |||:
Db         26 MTQSPSSLSASVGDRVTITCRAS---QNINNYLNWYQLKPGKAPNLLIYAASSLQSGVPS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  |    |||:  : :| | |:|   |:    ||||| : :  ||||||||||||
Db         83 RFSGSGSGTDFTLTISSLRPDDFATYYCQQSYNIPLTFGGGTNVEI-KRTVAAPSVFIFP 141

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 11
Q6PIL8
ID   Q6PIL8      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIL8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032451; AAH32451.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25834 MW;  6647A9E77A3C0053 CRC64;

  Query Match             63.4%;  Score 717.5;  DB 2;  Length 236;
  Best Local Similarity   69.6%;  Pred. No. 4.4e-55;
  Matches  151;  Conservative   18;  Mismatches   43;  Indels    5;  Gaps    4;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: |||| ||:||:|     :|:|  | |:||      || | ::|| |:|
Db         23 VLTQSPGTLSLSPGERATLSCRAS--QSLSSSYLAWYQQKPGQAPRLLIYGVSSRATGIP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWV-FGGGTKLTVLSRTVAAPSVFI 121
              ||||| |    |||: : || | |:|  : :   : || ||:| :  ||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSRPITFGQGTRLDI-KRTVAAPSVFI 139

Qy        122 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 199

Qy        182 TLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        200 TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 12
Q6GMX8
ID   Q6GMX8      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073764; AAH73764.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25707 MW;  4FC8E14B6559EFC9 CRC64;

  Query Match             63.2%;  Score 715.5;  DB 2;  Length 236;
  Best Local Similarity   69.3%;  Pred. No. 6.6e-55;
  Matches  149;  Conservative   19;  Mismatches   42;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  |::: | |: ||:|||:| |    |::  | |:||      ||  ::   |||:
Db         26 MTQSPSSVSASVGDRVTITCRASQG---ISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  |    |||: | || | |:|   :|  : || |||: :  ||||||||||
Db         83 RFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSFPFTFGPGTKVDI-KRTVAAPSVFIFP 141

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
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RESULT 13
Q6PIT5
ID   Q6PIT5      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIT5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC029444; AAH29444.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25741 MW;  BD50AF071FEEE351 CRC64;

  Query Match             62.2%;  Score 704;  DB 2;  Length 236;
  Best Local Similarity   69.1%;  Pred. No. 6.8e-54;
  Matches  152;  Conservative   15;  Mismatches   47;  Indels    6;  Gaps    4;

Qy          1 RSAV-VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              | |: :||  |:|: | || ||:|||:| |    |:   | |:||      ||   :
Db         21 RCAIQLTQSPSSLSASVGERVTITCRASQG---ISSALAWYQQKPGKPPKLLIYDASTME 77

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS 118
              |||:|||||  |    |||:  | || | ::|  : |    || || | :  |||||||
Db         78 SGVPSRFSGSGSGTHFTLTISSLQPEDFATFYCQQFKSYPRTFGQGTTLEI-KRTVAAPS 136

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 196

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||| ||||||||||
Db        197 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 14
Q6PIH4
ID   Q6PIH4      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034146; AAH34146.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25871 MW;  BE01A28CD06EEE26 CRC64;

  Query Match             62.1%;  Score 702.5;  DB 2;  Length 236;
  Best Local Similarity   68.8%;  Pred. No. 9.2e-54;
  Matches  148;  Conservative   18;  Mismatches   44;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  | |: | |: ||: ||:|      |::  | |:||      ||   :   |||:
Db         26 MTQSPSTLSASVGDRVTIACRAS---QWISDWLAWYQQKPGKAPKLLIYDASRLESGVPS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  | : :|||:| | :| | |:|  : |    || |||: :  ||||||||||||
Db         83 RFSGSGSGTEFSLTISGLQPDDFATYYCQPYNSNSPQFGQGTKVEI-KRTVAAPSVFIFP 141
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Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
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RESULT 15
Q8TCD0
ID Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC022362; AAH22362.1; -.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; 1I7Z.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match 61.6%; Score 697; DB 2; Length 239;
Best Local Similarity 67.4%; Pred. No. 2.8e-53;
Matches 149; Conservative 15; Mismatches 47; Indels 10; Gaps 5;

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              |:||   :|  : |:  :::|||:   | :  : | || |::|      ||   :||  |
Db         23 VMTQSPLSLPVTLGQPASISCRSTQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRDSG 82

Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFC---ALWYSCLWVFGGGTKLTVLSRTVAAP 117
              || ||||  |    | ||  : ||   |||     | |    || |||| :  ||||||
Db         83 VPDRFSGSGSGTDFTLKITRVEAEDVGVYFCMQGTHWPS---TFGQGTKLEI-KRTVAAP 138

Qy        118 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY 198

Qy        178 SLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||| ||||||||||
Db        199 SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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Job time : 113 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:28:46 ; Search time 114.5 Seconds
(without alignments)
736.365 Million cell updates/sec

Title: US-09-671-953B-7
Perfect score: 1134
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1132	99.8	218	4	AAB20360	Aab20360 Anti-chel
2	1122	98.9	218	4	AAB20359	Aab20359 Anti-chel
3	1113	98.1	218	4	AAB20358	Aab20358 Anti-chel
4	1083	95.5	218	8	ADQ98050	Adq98050 Chimeric
5	1082	95.4	218	8	ADQ98051	Adq98051 Chimeric
6	779	68.7	215	8	ADR23362	Adr23362 Human CD7
7	759.5	67.0	235	5	AAE27925	Aae27925 Human C2B
8	759.5	67.0	235	6	ABB82834	Abb82834 Antibody
9	759	66.9	213	8	ADL92471	Adl92471 Antibody
10	757	66.8	235	2	AAW82740	Aaw82740 Plasmid p
11	754.5	66.5	235	3	AAB08025	Aab08025 A dimeric
12	753	66.4	213	6	AAE34878	Aae34878 BIWA4/8 a
13	753	66.4	213	8	ADL15445	Adl15445 Humanised
14	753	66.4	213	8	ADO00853	Ado00853 Humanised
15	751	66.2	213	6	AAE35326	Aae35326 Humanised
16	751	66.2	213	6	AAE34877	Aae34877 BIWA4 ant
17	751	66.2	213	8	ADL15441	Adl15441 Humanised
18	751	66.2	213	8	ADO00849	Ado00849 Humanised
19	751	66.2	236	8	ADP79579	Adp79579 Chimeric
20	750	66.1	220	2	AAW07528	Aaw07528 Anti-HGF
21	746	65.8	215	8	ADQ31891	Adq31891 Antibody
22	744	65.6	215	8	ADQ31885	Adq31885 Antibody
23	743.5	65.6	234	5	AAO14066	Aao14066 Light cha
24	743.5	65.6	234	6	ABU08018	Abu08018 Human mon
25	743.5	65.6	234	7	ADF65776	Adf65776 Human mon
26	743.5	65.6	234	8	ADJ92516	Adj92516 Human SOJ
27	743	65.5	233	3	AAY93704	Aay93704 The kappa
28	743	65.5	233	3	AAY93731	Aay93731 The kappa
29	743	65.5	233	6	AAE35886	Aae35886 Human 4.8
30	743	65.5	239	8	ADK70470	Adk70470 Respirato
31	741.5	65.4	240	6	ABJ38595	Abj38595 Hepatitis
32	741	65.3	213	2	AAW05830	Aaw05830 Humanised
33	740.5	65.3	234	3	AAY92239	Aay92239 Human bon
34	739.5	65.2	234	6	ABP55483	Abp55483 CJRA05 pr
35	739	65.2	215	8	ADQ16702	Adq16702 Modified
36	738	65.1	213	6	AAE33521	Aae33521 Human AQC
37	738	65.1	232	8	ADP79583	Adp79583 2H7.v16 L
38	736	64.9	235	2	AAW06180	Aaw06180 Humanised
39	736	64.9	236	2	AAY34096	Aay34096 Partial a
40	735.5	64.9	214	8	ADH34591	Adh34591 023 light
41	735.5	64.9	349	2	AAR12128	Aar12128 1B1 IgG a
42	735.5	64.9	414	2	AAR13111	Aar13111 1B1 IgG a
43	735.5	64.9	414	2	AAR13018	Aar13018 1B1 IgG a
44	735	64.8	213	4	AAB83157	Aab83157 Gangliosi
45	735	64.8	215	6	ABR01469	Abr01469 Human ant

ALIGNMENTS

RESULT 1
AAB20360
ID AAB20360 standard; protein; 218 AA.
XX
AC AAB20360;
XX
DT 11-JUN-2001 (first entry)
XX
DE Anti-chelate antibody CHA255 light chain mutant S95C.
XX
KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
KW cancer; therapy; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX

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FT	Region	24. .37
FT		/label= CDR1
FT		/note= "complementarity determining region 1"
FT	Region	38. .52
FT		/label= FR2
FT		/note= "framework region 2"
FT	Region	53. .59
FT		/label= CDR2
FT		/note= "complementarity determining region 2"
FT	Region	60. .92
FT		/label= FR3
FT		/note= "framework region 3"
FT	Region	93. .100
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FT		/note= "complementarity determining region 3"
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FT		/note= "replaces Ser of wild-type sequence"
FT	Misc-difference	100
FT		/note= "encoded by GTR"
FT	Region	101. .131
FT		/label= FR4
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FT	Misc-difference	112
FT		/note= "encoded by CGW"
FT	Misc-difference	113
FT		/note= "encoded by ACK"
FT	Misc-difference	206
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PN   WO200122922-A2.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026619.
XX
PR   27-SEP-1999;   99US-0156194P.
PR   31-MAY-2000; 2000US-0208684P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Meares C,  Chmura A;
XX
DR   WPI; 2001-244971/25.
DR   N-PSDB; AAF30635.
XX
PT   Nucleic acid encoding a mutant antibody comprising a reactive site that
PT   specifically binds to a metal chelate useful as analytical agents and in
PT   clinical diagnosis, as well as in the treatment of disease, particularly
PT   cancer.
XX
PS   Disclosure; Fig 14; 100pp; English.
XX
CC   The invention provides a mutant antibody comprising a reactive site that
CC   is not present in the wild-type of the antibody. The antibody also has a
CC   complementarity determining region (CDR) that specifically binds to a
CC   metal chelate against which the wild-type antibody is raised. The
CC   reactive site of the mutant antibody is in a position proximate to or
CC   within the CDR, such that the chelate and the antibody are able to form a
CC   covalent bond. The present sequence is that of the light chain variable
CC   region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C
CC   mutation. As an example of the method of the invention, rational computer
CC   -aided design was used to develop an indium-EDTA chelate to covalently
CC   bind to CHA255 in vivo. The premise was to allow the chelate to bind non-
CC   covalently to CHA255 bound to a tumour and then to covalently attach the
CC   chelate to the antibody, thereby trapping it at the tumour site. This
CC   involved cloning the variable domains of CHA255 to construct a
CC   human/mouse chimeric Fab fragment that could be expressed in Escherichia
CC   coli, and the synthesis and screening of benzyl-EDTA chelates carrying
CC   weakly electrophilic groups capable of conjugation of the antibody in
CC   vivo. This Fab can be conjugated to a targeting moiety when desired. A
CC   reactive site was incorporated into the antibody by engineering a Cys
CC   residue at location Asn-96 or Ser-95 of the light chain, near the region
CC   of the antibody to which the chelate bound. This was accomplished by site
CC   -directed mutagenesis of a nucleic acid encoding the wild-type of the
CC   anti-chelate antibody
XX
SQ   Sequence 218 AA;

  Query Match             99.8%;  Score 1132;  DB 4;  Length 218;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-79;
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Qy          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60

Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||||||||||||
Db        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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RESULT 2
AAB20359
ID   AAB20359 standard; protein; 218 AA.
XX
AC   AAB20359;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Anti-chelate antibody CHA255 light chain.
XX
KW   Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
KW   cancer; therapy.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .23
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          24. .37
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          38. .52
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          53. .59
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          60. .92
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          93. .100
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Misc-difference 100
FT                   /note= "encoded by GTR"
FT   Region          101. .131
FT                   /label= FR4
FT                   /note= "framework region 4"
FT   Misc-difference 112
FT                   /note= "encoded by CGW"
FT   Misc-difference 113
FT                   /note= "encoded by ACK"
FT   Misc-difference 206
FT                   /note= "encoded by AGY"
FT   Misc-difference 207
FT                   /note= "encoded by TYG"
XX
PN   WO200122922-A2.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026619.
XX
PR   27-SEP-1999;   99US-0156194P.
PR   31-MAY-2000; 2000US-0208684P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Meares C,  Chmura A;
XX
DR   WPI; 2001-244971/25.
DR   N-PSDB; AAF30634.
XX
PT   Nucleic acid encoding a mutant antibody comprising a reactive site that
PT   specifically binds to a metal chelate useful as analytical agents and in
PT   clinical diagnosis, as well as in the treatment of disease, particularly
PT   cancer.
XX
PS   Disclosure; Fig 13; 100pp; English.
XX
CC   The invention provides a mutant antibody comprising a reactive site that
CC   is not present in the wild-type of the antibody. The antibody also has a
```

```
CC   complementarity determining region (CDR) that specifically binds to a
CC   metal chelate against which the wild-type antibody is raised. The
CC   reactive site of the mutant antibody is in a position proximate to or
CC   within the CDR, such that the chelate and the antibody are able to form a
CC   covalent bond. The present sequence is that of the light chain of anti-
CC   indium-EDTA monoclonal antibody CHA255. As an example of the method of
CC   the invention, rational computer-aided design was used to develop an
CC   indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was
CC   to allow the chelate to bind non-covalently to CHA255 bound to a tumour
CC   and then to covalently attach the chelate to the antibody, thereby
CC   trapping it at the tumour site. This involved cloning the variable
CC   domains of CHA255 to construct a human/mouse chimeric Fab fragment that
CC   could be expressed in Escherichia coli, and the synthesis and screening
CC   of benzyl-EDTA chelates carrying weakly electrophilic groups capable of
CC   conjugation of the antibody in vivo. This Fab can be conjugated to a
CC   targeting moiety when desired. A reactive site was incorporated into the
CC   antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the
CC   light chain, near the region of the antibody to which the chelate bound.
CC   This was accomplished by site-directed mutagenesis of a nucleic acid
CC   encoding the wild-type of the anti-chelate antibody
XX
SQ   Sequence 218 AA;

  Query Match             98.9%;  Score 1122;  DB 4;  Length 218;
  Best Local Similarity   99.5%;  Pred. No. 2.3e-78;
  Matches  217;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60

Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSNLWVFGGGTKLTVLSRTVAAPSVF 120

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||||||||||||
Db        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218


RESULT 3
AAB20358
ID   AAB20358 standard; protein; 218 AA.
XX
AC   AAB20358;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Anti-chelate antibody CHA255 light chain mutant N96C.
XX
KW   Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
KW   cancer; therapy; mutant; mutein.
XX
OS   Mus musculus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .23
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          24. .37
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          38. .52
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          53. .59
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          60. .92
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          93. .100
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Misc-difference 96
FT                   /note= "replaces Asn of wild-type sequence"
FT   Misc-difference 100
FT                   /note= "encoded by GTR"
FT   Region          101. .131
FT                   /label= FR4
FT                   /note= "framework region 4"
FT   Misc-difference 112
FT                   /note= "encoded by CGW"
FT   Misc-difference 113
FT                   /note= "encoded by ACK"
FT   Misc-difference 206
FT                   /note= "encoded by AGY"
FT   Misc-difference 207
FT                   /note= "encoded by TYG"
XX
PN   WO200122922-A2.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-US026619.
XX
PR   27-SEP-1999;   99US-0156194P.
PR   31-MAY-2000; 2000US-0208684P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Meares C,  Chmura A;
XX
DR   WPI; 2001-244971/25.
DR   N-PSDB; AAF30633.
XX
PT   Nucleic acid encoding a mutant antibody comprising a reactive site that
PT   specifically binds to a metal chelate useful as analytical agents and in
PT   clinical diagnosis, as well as in the treatment of disease, particularly
PT   cancer.
XX
PS   Disclosure; Fig 12; 100pp; English.
XX
CC   The invention provides a mutant antibody comprising a reactive site that
CC   is not present in the wild-type of the antibody. The antibody also has a
CC   complementarity determining region (CDR) that specifically binds to a
CC   metal chelate against which the wild-type antibody is raised. The
CC   reactive site of the mutant antibody is in a position proximate to or
CC   within the CDR, such that the chelate and the antibody are able to form a
CC   covalent bond. The present sequence is that of the light chain variable
CC   region of anti-indium-EDTA monoclonal antibody CHA255, carrying an N96C
CC   mutation. As an example of the method of the invention, rational computer
CC   -aided design was used to develop an indium-EDTA chelate to covalently
CC   bind to CHA255 in vivo. The premise was to allow the chelate to bind non-
CC   covalently to CHA255 bound to a tumour and then to covalently attach the
CC   chelate to the antibody, thereby trapping it at the tumour site. This
CC   involved cloning the variable domains of CHA255 to construct a
CC   human/mouse chimeric Fab fragment that could be expressed in Escherichia
CC   coli, and the synthesis and screening of benzyl-EDTA chelates carrying
CC   weakly electrophilic groups capable of conjugation of the antibody in
CC   vivo. This Fab can be conjugated to a targeting moiety when desired. A
CC   reactive site was incorporated into the antibody by engineering a Cys
CC   residue at location Asn-96 or Ser-95 of the light chain, near the region
CC   of the antibody to which the chelate bound. This was accomplished by site
CC   -directed mutagenesis of a nucleic acid encoding the wild-type of the
CC   anti-chelate antibody
XX
SQ   Sequence 218 AA;

  Query Match             98.1%;  Score 1113;  DB 4;  Length 218;
  Best Local Similarity   99.1%;  Pred. No. 1.1e-77;
```

```
  Matches  216;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60

Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
              |||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||||||||||||
Db        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218


RESULT 4
ADQ98050
ID   ADQ98050 standard; protein; 218 AA.
XX
AC   ADQ98050;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Chimeric murine 2D12.5 variable light chain fused to human TTCL protein.
XX
KW   murine; mouse; chimeric; human; TTCL; tetanus toxin;
KW   magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
KW   single photon emission tomography; SPET; cancer; cytostatic;
KW   immunosuppressive; multi-functional antibody; metal chelate;
KW   antigen recognition domain; in vivo imaging;
KW   cell-antibody-metal chelate complex; emission tomography.
XX
OS   Mus musculus.
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO2004065569-A2.
XX
PD   05-AUG-2004.
XX
PF   23-JAN-2004; 2004WO-US001808.
XX
PR   23-JAN-2003; 2003US-00350555.
PR   22-JUL-2003; 2003US-00625047.
PR   31-JUL-2003; 2003US-00631258.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Meares C,  Corneillie T;
XX
DR   WPI; 2004-580725/56.
DR   N-PSDB; ADQ98054.
XX
PT   Novel mutant antibody comprising reactive site not present in wild-type
PT   of antibody and antigen recognition domain that recognizes macrocyclic
PT   metal chelate having four nitrogen atoms, useful for treating cancer or
PT   autoimmune diseases.
XX
PS   Claim 41; SEQ ID NO 27; 208pp; English.
XX
CC   This invention relates to multi-functional antibodies that recognise
CC   chelating agents and metal chelates, particularly macrocyclic metal
CC   chelates. Specifically, it refers to an antibody that comprises a metal
CC   chelate bound to an antigen recognition domain, where the metal chelate
CC   has a reactive functional group of complementary reactivity to the
CC   reactive site of the antibody. This reactive site is the side chain of a
CC   naturally occurring amino acid e.g. the -SH group side chain of a
CC   cysteine residue (not present in the wild type) which can be used to form
CC   a covalent bond between the reactive site of the antibody and the
CC   reactive functional group of the metal chelate. The present invention
CC   describes using these antibodies for in vivo imaging where the antibody
CC   comprises a targeting moiety that binds specifically to a cell via a cell
CC   surface receptor or antigen thus forming a cell-mutant antibody complex.
CC   On addition of the metal chelate, a cell-antibody-metal chelate complex
CC   is formed that can be detected using emission tomography, magnetic
CC   resonance imaging, lanthanide luminescence, gamma-emissions or single
CC   photon emission tomography (SPET). As such, this method is useful for
CC   treating a subject with cancer and pharmaceutical compositions exhibit
CC   cytostatic and immunosuppressive activities. This polypeptide sequence is
CC   the chimeric murine antibody 2D12.5 variable light chain protein fused to
CC   the human anti-tetanus toxin antibody kappa light chain constant region
CC   of the invention.
XX
SQ   Sequence 218 AA;

  Query Match             95.5%;  Score 1083;  DB 8;  Length 218;
  Best Local Similarity   95.9%;  Pred. No. 2.3e-75;
  Matches  209;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
              |||||||||||||||||||||||| |||||||||||||||||||||||| ||| ||
Db          1 RSAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGNNNRPPG 60

Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
              |||||||||||||||| | |||||| ||||||| | ||||||||||||||||||||||||
Db         61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        181 STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218


RESULT 5
ADQ98051
ID   ADQ98051 standard; protein; 218 AA.
XX
AC   ADQ98051;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Chimeric N53C murine 2D12.5 light chain variable and human TTCL protein.
XX
KW   murine; mouse; chimeric; human; TTCL; tetanus toxin;
KW   magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
KW   single photon emission tomography; SPET; cancer; cytostatic;
KW   immunosuppressive; multi-functional antibody; metal chelate;
KW   antigen recognition domain; in vivo imaging;
KW   cell-antibody-metal chelate complex; emission tomography; mutant; mutein.
XX
OS   Mus musculus.
OS   Homo sapiens.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 55
FT                   /note= "Wild type Asn substituted for Cys"
XX
PN   WO2004065569-A2.
XX
PD   05-AUG-2004.
XX
PF   23-JAN-2004; 2004WO-US001808.
XX
PR   23-JAN-2003; 2003US-00350555.
PR   22-JUL-2003; 2003US-00625047.
PR   31-JUL-2003; 2003US-00631258.
XX
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PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Meares C,  Corneillie T;
XX
DR   WPI; 2004-580725/56.
DR   N-PSDB; ADQ98055.
XX
PT   Novel mutant antibody comprising reactive site not present in wild-type
PT   of antibody and antigen recognition domain that recognizes macrocyclic
PT   metal chelate having four nitrogen atoms, useful for treating cancer or
PT   autoimmune diseases.
XX
PS   Claim 41; SEQ ID NO 28; 208pp; English.
XX
CC   This invention relates to multi-functional antibodies that recognise
CC   chelating agents and metal chelates, particularly macrocyclic metal
CC   chelates. Specifically, it refers to an antibody that comprises a metal
CC   chelate bound to an antigen recognition domain, where the metal chelate
CC   has a reactive functional group of complementary reactivity to the
CC   reactive site of the antibody. This reactive site is the side chain of a
CC   naturally occurring amino acid e.g. the -SH group side chain of a
CC   cysteine residue (not present in the wild type) which can be used to form
CC   a covalent bond between the reactive site of the antibody and the
CC   reactive functional group of the metal chelate. The present invention
CC   describes using these antibodies for in vivo imaging where the antibody
CC   comprises a targeting moiety that binds specifically to a cell via a cell
CC   surface receptor or antigen thus forming a cell-mutant antibody complex.
CC   On addition of the metal chelate, a cell-antibody-metal chelate complex
CC   is formed that can be detected using emission tomography, magnetic
CC   resonance imaging, lanthanide luminescence, gamma-emissions or single
CC   photon emission tomography (SPET). As such, this method is useful for
CC   treating a subject with cancer and pharmaceutical compositions exhibit
CC   cytostatic and immunosuppressive activities. This polypeptide sequence is
CC   the chimeric mutant N53C murine antibody 2D12.5 variable light chain
CC   protein fused to the human anti-tetanus toxin antibody kappa light chain
CC   constant region of the invention.
XX
SQ   Sequence 218 AA;

  Query Match             95.4%;  Score 1082;  DB 8;  Length 218;
  Best Local Similarity   95.9%;  Pred. No. 2.7e-75;
  Matches  209;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||| ||| ||
Db          1 RSAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGCNNRPPG 60

Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
              |||||||||||||||| | |||||| ||||||| | ||||||||||||||||||||||||
Db         61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||| ||||||||||
Db        181 STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218


RESULT 6
ADR23362
ID   ADR23362 standard; protein; 215 AA.
XX
AC   ADR23362;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human CD72-targeted IgG1 light chain.
XX
KW   Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;
KW   immunosuppressive; cancer; autoimmune disease; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .109
FT                   /label= V_region
FT   Region          110. .215
FT                   /label= C_region
XX
PN   WO2004067569-A1.
XX
PD   12-AUG-2004.
XX
PF   27-JAN-2003; 2003WO-EP050004.
XX
PR   27-JAN-2003; 2003WO-EP050004.
XX
PA   (CRUC-) CRUCELL HOLLAND BV.
XX
PI   Bakker ABH,  Marissen WE;
XX
DR   WPI; 2004-580978/56.
DR   N-PSDB; ADR23361.
XX
PT   New internalizing human binding molecules capable of specifically binding
PT   to CD72, useful for diagnosing and/or treating B-cell associated
PT   diseases, such as cancer or autoimmune disorders.
XX
PS   Example 5; SEQ ID NO 54; 174pp; English.
XX
CC   The present sequence is the protein sequence of the light chain of human
CC   IgG1 antibody 025, which specifically recognises human B cell associated
CC   antigen CD72. An scFv ADR23324 selected from an antibody phage display
CC   library was shown to specifically recognise the human CD72 receptor. The
CC   scFv was recloned in IgG expression vector C01 using primers designed to
CC   restore complete human frameworks, thereby generating antibody 025. Such
CC   anti-CD72 immunoglobulins or their antigen-binding fragments can be used
CC   as internalising human binding molecules of the invention. These
CC   internalising human binding molecules are capable of (specifically)
CC   binding to CD72 or its antigenic determinant, and preferably bind to CD72
CC   associated with cells. Upon binding to CD72 present on the surface of
CC   target cells, the binding molecules internalise. In addition to the
CC   internalising human binding molecules, the invention provides
CC   immunoconjugates comprising an internalising human binding molecule and a
CC   tag (toxic substance, radioactive substance, liposome and/or enzyme),
CC   nucleic acids encoding these, and compositions comprising them. The
CC   internalising human binding molecule, immunoconjugate, nucleic acid
CC   molecule or composition can be used in the diagnosis and/or treatment of
CC   a B cell associated disorder or disease, especially a B cell associated
CC   cancer and B cell associated autoimmune disorder (claimed).
XX
SQ   Sequence 215 AA;

  Query Match             68.7%;  Score 779;  DB 8;  Length 215;
  Best Local Similarity   72.3%;  Pred. No. 5.4e-52;
  Matches  162;  Conservative   15;  Mismatches   31;  Indels   16;  Gaps    4;

Qy          2 SAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 61
              |: :||: |:: : |:|| :||:    |    | ||:| |:||       :| | |||  |:
Db          1 SSELTQDPAVSVALGQTVRITCQ---GDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGI 57

Qy         62 PARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNL-------WVFGGGTKLTVLSRTV 114
              | |||||  |: |:||||||| |||| |     |||          |||||||||||  ||
Db         58 PDRFSGSSSGNTASLTITGAQAEDEADY-----YCNSRDSSGNHVVFGGGTKLTVLG-TV 111

Qy        115 AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD 171

Qy        175 STYSLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||||| ||||||||||
Db        172 STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
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RESULT 7
AAE27925
ID   AAE27925 standard; protein; 235 AA.
XX
AC   AAE27925;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human C2B8 antibody light chain protein.
XX
KW   Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
KW   neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
KW   non-Hodgkin's lymphoma; haematologic malignancy; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200260955-A2.
XX
PD   08-AUG-2002.
XX
PF   29-JAN-2002; 2002WO-US002373.
XX
PR   29-JAN-2001; 2001US-0264318P.
PR   16-NOV-2001; 2001US-0331481P.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Braslawsky GR,  Hanna N,  Chinn P;
XX
DR   WPI; 2002-698547/75.
DR   N-PSDB; AAD45754.
XX
PT   Novel domain deleted CC49 antibody reactive with tumor associated antigen
PT   -72, or C2B8 antibody reactive with CD20, useful for treating
PT   myelosuppressed patient suffering from a neoplastic disorder.
XX
PS   Example 1; Fig 3B; 74pp; English.
XX
CC   The present invention relates to domain deleted CC49 or C2B8 antibodies.
CC   Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
CC   deleted sequence in which CH2 domain has been deleted and are reactive
CC   with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
CC   with CD20 and comprise a heavy chain having a sequence of a derived
CC   domain deleted C2B8 construct where the CH2 domain has been deleted.
CC   Sequences of the invention are useful for imaging a neoplasm. They are
CC   also useful for treating myelosuppressed patients suffering from
CC   neoplastic disorder such as haematologic neoplasm, preferably non-
CC   Hodgkin's lymphoma. Antibodies of the invention are also used to treat
CC   neoplastic disorder, colon cancer and haematologic malignancy. They are
CC   useful for reducing tumour size, inhibiting tumour growth and/or
CC   prolonging the survival time of tumour-bearing animals and for treating
CC   tumours. The present sequence is human C2B8 light chain protein. This
CC   sequence is used in the exemplification of the invention
XX
SQ   Sequence 235 AA;

  Query Match             67.0%;  Score 759.5;  DB 5;  Length 235;
  Best Local Similarity   70.5%;  Pred. No. 1.9e-50;
  Matches  155;  Conservative   16;  Mismatches   42;  Indels    7;  Gaps    3;

Qy          1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              |  :|  :|   |: |||| ||:|||:|    :: :| :| |:||       |  |:| |
Db         21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLA 76

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS 118
               ||| |||||  |   :|||:  : || | |:|  |  |   ||||||| :  |||||||
Db         77 SGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEI-KRTVAAPS 135

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||||||| ||||||||||
Db        196 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 8
ABB82834
ID   ABB82834 standard; protein; 235 AA.
XX
AC   ABB82834;
XX
DT   31-MAR-2003  (first entry)
XX
DE   Antibody C2B8 light chain.
XX
KW   C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
KW   vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
KW   thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
KW   neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
KW   dermatological; immunosuppressive; antiinflammatory.
XX
OS   Homo sapiens.
XX
PN   WO200296948-A2.
XX
PD   05-DEC-2002.
XX
PF   29-JAN-2002; 2002WO-US002374.
XX
PR   29-JAN-2001; 2001US-0264318P.
PR   16-NOV-2001; 2001US-0331481P.
PR   21-DEC-2001; 2001US-0341858P.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Braslawsky GR,  Hanna N,  Chinn P,  Hariharan K;
XX
DR   WPI; 2003-140446/13.
DR   N-PSDB; ABZ24018.
XX
PT   Novel dimeric antibody useful for treating immune disorder and neoplastic
PT   disorder, has several non-covalently associated monomeric subunits.
XX
PS   Example 1; Fig 3B; 78pp; English.
XX
CC   The invention relates to a dimeric antibody (I) comprising several
CC   monomeric subunits, where the monomeric subunits are non-covalently
CC   associated. (I) is useful for treating a disorder, especially immune
CC   disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
CC   resistant Hodgkin's disease high grade, low grade and intermediate grade
CC   non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
CC   lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
CC   lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
CC   AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
CC   lymphoadenopathy, small lymphocytic, follicular, diffuse large cell,
CC   diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
CC   small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
CC   cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
CC   detailed description of the various uses of (I)). The present sequence
CC   represents the antibody C2B8 light chain
XX
SQ   Sequence 235 AA;

  Query Match             67.0%;  Score 759.5;  DB 6;  Length 235;
  Best Local Similarity   70.5%;  Pred. No. 1.9e-50;
  Matches  155;  Conservative   16;  Mismatches   42;  Indels    7;  Gaps    3;

Qy          1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              |  :|  :|   |: |||| ||:|||:|    :: :| :| |:||       |  |:| |
Db         21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLA 76

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS 118
               ||| |||||  |   :|||:  : || | |:|  |  |   ||||||| :  |||||||
Db         77 SGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEI-KRTVAAPS 135
```

```
Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||| ||||||||||
Db        196 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
```

RESULT 9
ADL92471
ID ADL92471 standard; protein; 213 AA.
XX
AC ADL92471;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antibody "Rituximab" light chain sequence.
XX
KW cytostatic; antiinflammatory; cardiovascular; gene therapy; antibody; Fc;
KW agriculture; industrial application.
XX
OS Homo sapiens.
XX
PN WO2004029207-A2.
XX
PD 08-APR-2004.
XX
PF 26-SEP-2003; 2003WO-US030249.
XX
PR 27-SEP-2002; 2002US-0414433P.
PR 23-JAN-2003; 2003US-0442301P.
PR 02-MAY-2003; 2003US-0467606P.
PR 12-JUN-2003; 2003US-0477839P.
XX
PA (XENC-) XENCOR.
XX
PI Lazar GA, Chirino AJ, Dang W, Desjarlais JR, Doberstein SK;
PI Hayes RJ, Karki SB, Vafa O;
XX
DR WPI; 2004-316096/29.
XX
PT New optimized Fc variant antibody useful for diagnosing or treating
PT diseases (e.g. cancer, inflammation or cardiovascular diseases), in
PT research and in agricultural or industrial applications.
XX
PS Example 12; Fig 31a; 192pp; English.
XX
CC The invention relates to an antibody comprising an Fc variant portion
CC having an amino acid modification in the Fc region of the parent Fc
CC polypeptide, where the Fc variant modulates binding to an Fc-gamma-R
CC compared to the parent Fc polypeptide. The antibody may also be used in
CC research and in agricultural or industrial applications. This sequence
CC corresponds to the light chain of the antibody "Rituximab" as an example
CC of an antibody of the invention.
XX
SQ Sequence 213 AA;

```
  Query Match             66.9%;  Score 759;  DB 8;  Length 213;
  Best Local Similarity   71.8%;  Pred. No. 1.9e-50;
  Matches  155;  Conservative   16;  Mismatches   39;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |::|  | |: |||| ||:|||:|    :: :| :| |:||       |  |:| | |||
Db          3 VLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
               |||||  |   :|||:  : || | |:|  |  |   ||||||| :  ||||||||||
Db         59 VRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
```

RESULT 10
AAW82740
ID AAW82740 standard; protein; 235 AA.
XX
AC AAW82740;
XX
DT 10-MAY-1999 (first entry)
XX
DE Plasmid pNG3/A5B7VK-HuCK-NEO protein.
XX
KW Conjugate; cell targeting; cytotoxic drug; prodrug therapy system;
KW prodrug-converting enzyme; cell surface antigen; treatment; cancer;
KW inflammation; rheumatoid arthritis; antibody.
XX
OS Synthetic.
XX
PN WO9851787-A2.
XX
PD 19-NOV-1998.
XX
PF 05-MAY-1998; 98WO-GB001294.
XX
PR 10-MAY-1997; 97GB-00009421.
XX
PA (ZENE) ZENECA LTD.
XX
PI Emery SC, Blakey DC;
XX
DR WPI; 1999-059700/05.
DR N-PSDB; AAV72047.
XX
PT New gene construct expressing conjugate of targetting agent and prodrug-
PT converting enzyme - useful for, e.g. targetted production of cytotoxic
PT drug in vivo, especially for treatment of cancer.
XX
PS Example 1f; Page 70; 100pp; English.
XX
CC This sequence is used in a method for obtaining a novel gene construct
CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-
CC targeting group (I) and a heterologous prodrug-converting enzyme (II),
CC and (B) is directed to leave the cell for selective localisation at a
CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target
CC site, then administration of (III) is used for targeted release of
CC cytotoxic drug, specifically for treating cancer but also inflammation
CC such as rheumatoid arthritis. In situ generation of the targeting
CC antibody increases selectivity, reducing side effects at normal tissue.
CC The method is applicable to any antibody-directed enzyme prodrug therapy
CC system
XX
SQ Sequence 235 AA;

```
  Query Match             66.8%;  Score 757;  DB 2;  Length 235;
  Best Local Similarity   71.8%;  Pred. No. 3e-50;
  Matches  155;  Conservative   15;  Mismatches   40;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |::|  | |: |||| ||:|||:|    :: :| :| |:||       |  |:| | |||
Db         25 VLSQSPAILSASPGEKVTMTCRAS----SSVTYIHWYQQKPGSSPKSWIYATSNLASGVP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
               ||||||  |   :|||:  : || | |:|  |       ||||||| :  ||||||||||
Db         81 ARFSGSGSGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
```

```
Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
```

RESULT 11
AAB08025
ID AAB08025 standard; protein; 235 AA.
XX
AC AAB08025;
XX
DT 12-SEP-2003 (revised)
DT 14-NOV-2000 (first entry)
XX
DE A dimeric anti-CD20 light chain polypeptide.
XX
KW Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;
KW complement system; Fcgamma receptor; cytotoxic effector cell;
KW host immune cell; programmed cell death; allergic disorder; cancer;
KW autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease;
KW allergic bronchopulmonary aspergillosis; allergic rhinitis;
KW Graves's disease; food allergy; allergic contact dermatitis; cancer;
KW B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis;
KW pigeon breeder's disease; hepatitis; leprosy; Lyme disease;
KW diabetes mellitus; candidiasis; aplastic anaemia.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FH Key   Location/Qualifiers
FT Peptide   1. .22
FT   /note= "signal peptide"
FT Protein   23. .128
FT   /note= "murine anti-human CD20 variable light chain"
FT Protein   129. .235
FT   /note= "human kappa light chain constant region"
XX
PN WO200044788-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US001893.
XX
PR 28-JAN-1999; 99US-00238741.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Braslawsky GR, Hanna N, Hariharan K, Labarre MJ, Huynh TB;
XX
DR WPI; 2000-514811/46.
DR N-PSDB; AAA63530.
XX
PT Genetically engineering immunoglobulin (Ig) G/IgG dimers for the
PT treatment of cancers, allergic disorders and autoimmune conditions.
XX
PS Example 1; Fig 1A-B; 65pp; English.
XX
CC The present sequence represents a dimeric anti-CD20 light chain
CC polypeptide. The dimeric immunoglobulin is used in the method of the
CC invention. The specification describes a method for producing an
CC immunoglobulin (Ig) G/IgG dimer. The method comprises genetically
CC engineering a monoclonal antibody to introduce a cysteine molecule which
CC inhibits formation of intramolecular disulphide bridges between sister
CC heavy chains on the same antibody molecule. The dimer is a homodimer or
CC heterodimer that is capable of activating components of the complement
CC system, and has the ability to activate and kill cells via the complement
CC cascade. The dimer is also capable of binding to Fcgamma receptors on
CC cytotoxic effector cells and on host immune cells, and is capable of
CC initiating programmed cell death. The IgG/IgG dimers may be used to treat
CC allergic disorders, cancers and autoimmune diseases such as allergic
CC asthma, allergic bronchopulmonary aspergillosis, allergic rhinitis,
CC atopic dermatitis, Crohn's disease, Graves's disease, food allergies,
CC allergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They
CC may also be used to treat a range of other diseases and disorders such as
CC rheumatoid arthritis, ulcerative colitis, psoriasis, pigeon breeder's
CC disease, hepatitis, leprosy, Lyme disease, diabetes mellitus, candidiasis
CC and aplastic anaemia. They are also useful for inducing hyper-cross-
CC linking of membrane antigens and for the preferential killing of selected
CC cell populations. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 235 AA;

  Query Match   66.5%; Score 754.5; DB 3; Length 235;
  Best Local Similarity   70.0%; Pred. No. 4.6e-50;
  Matches 154; Conservative   16; Mismatches   43; Indels   7; Gaps   3;

```
Qy          1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              |  :|  :|   |: |||| ||:|||:|    :: :| :| |:||       |  |:| |
Db         21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKRWIYATSNLA 76

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS 118
              ||| |||||  |   :|||:  : || | |:|  |  |   |||| || :  |||||||
Db         77 SGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGAKLEI-KRTVAAPS 135

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        196 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
```

RESULT 12
AAE34878
ID AAE34878 standard; protein; 213 AA.
XX
AC AAE34878;
XX
DT 28-MAY-2003 (first entry)
XX
DE BIWA4/8 antibody light chain mature protein.
XX
KW BIWA8 antibody; heavy chain variable region; light chain variable region;
KW VH; VL; CD44v6; medicament; cancer; antibody therapy.
XX
OS Unidentified.
XX
PN WO200294879-A1.
XX
PD 28-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-EP005467.
XX
PR 18-MAY-2001; 2001EP-00112237.
PR 26-SEP-2001; 2001US-0325147P.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Adolf G, Ostermann E, Patzelt E, Sproll M, Heider K;
PI Miglietta JJ, Van Dongen AAMS;
XX
DR WPI; 2003-129413/12.
DR N-PSDB; AAD53214, AAD53217.
XX
PT New antibodies specific for an epitope coded by the variant exon of the
PT CD44 gene, useful for treating cancer, including non-small cell lung,
PT breast, head and neck, ovarian and lung cancer.
XX
PS Claim 26; Col 44; 78pp; English.
XX
CC The present invention relates to novel antibody molecules comprising a
CC variable region of the heavy (VH) and/or light chain (VL) of CD44v6

CC specific humanised antibody called BIWA8 and BIWA4. Sequences of the
CC invention are useful for manufacturing a medicament and for treating
CC cancer including colorectum, non-small cell lung, breast, head and neck,
CC ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the
CC brain. They are also useful in antibody therapy. The present sequence is
CC BIWA4/8 antibody light chain mature protein. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 213 AA;

```
  Query Match             66.4%;  Score 753;  DB 6;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 5.4e-50;
  Matches  156;  Conservative   14;  Mismatches   40;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: |||| ||:| :|    :: ||  |:|:||      ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWLQQKPGQAPRILIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  |  |   ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
```

RESULT 13
ADL15445
ID ADL15445 standard; protein; 213 AA.
XX
AC ADL15445;
XX
DT 06-MAY-2004 (first entry)
XX
DE Humanised murine antibody BIWA8 light chain protein.
XX
KW cancer; cell differentiation antigen-44; CD44; cytotoxic;
KW chemotherapeutic agent; cytostatic; head; neck squamous cell carcinoma;
KW oesophagus; lung; skin; cervix; breast adenocarcinoma; pancreas; colon;
KW stomach; human; murine; mouse; antibody; BIWA8; light chain.
XX
OS Homo sapiens.
OS Mus sp.
XX
PN EP1391213-A1.
XX
PD 25-FEB-2004.
XX
PF 21-AUG-2002; 2002EP-00018686.
XX
PR 21-AUG-2002; 2002EP-00018686.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX
PI Adolf G, Baum A, Heider K;
XX
DR WPI; 2004-249201/24.
DR N-PSDB; ADL15446.
XX
PT Use of a conjugate of antibody to specified cell differentiation antigen
PT with cytotoxic compound in the preparation of pharmaceutical composition
PT for the treatment of cancer.
XX
PS Claim 7; SEQ ID NO 8; 52pp; English.
XX
CC The invention relates to a novel method for the preparation of a
CC pharmaceutical composition for the treatment of cancer whereby a
CC conjugate of a specific antibody to cell differentiation antigen-44
CC (CD44) with a cytotoxic compound is used optionally in combination with a
CC chemotherapeutic agent. The method of the invention has cytostatic
CC applications and may be useful in the preparation of a pharmaceutical
CC composition for the treatment of cancer, particularly head and neck
CC squamous cell carcinoma, oesophagus squamous cell carcinoma, lung
CC squamous cell carcinoma, skin squamous cell carcinoma, cervix squamous
CC cell carcinoma, breast adenocarcinoma, lung adenocarcinoma, pancreas
CC adenocarcinoma, colon adenocarcinoma and stomach adenocarcinoma. The
CC current sequence is that of the humanised murine antibody BIWA8 light
CC chain protein of the invention.
XX
SQ Sequence 213 AA;

```
  Query Match             66.4%;  Score 753;  DB 8;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 5.4e-50;
  Matches  156;  Conservative   14;  Mismatches   40;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: |||| ||:| :|    :: ||  |:|:||      ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWLQQKPGQAPRILIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  |  |   ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
```

RESULT 14
ADO00853
ID ADO00853 standard; protein; 213 AA.
XX
AC ADO00853;
XX
DT 29-JUL-2004 (first entry)
XX
DE Humanised murine antibody BIWA 8 light chain protein SEQ ID NO:8.
XX
KW CD44 specific antibody; CD44; cancer; radiotherapy;
KW CD44v6 specific antibody; maytansinoid; radioimmunotherapeutic;
KW cytostatic; immunostimulator; head and neck squamous cell carcinoma;
KW oesophagus squamous cell carcinoma; lung squamous cell carcinoma;
KW skin squamous cell carcinoma; cervix squamous cell carcinoma;
KW breast adenocarcinoma; lung adenocarcinoma; pancreas adenocarcinoma;
KW colon adenocarcinoma; stomach adenocarcinoma;
KW humanised murine antibody BIWA 8 light chain.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX
PN EP1417974-A1.
XX
PD 12-MAY-2004.
XX
PF 08-NOV-2002; 2002EP-00024881.
XX
PR 08-NOV-2002; 2002EP-00024881.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX
DR WPI; 2004-378705/36.
DR N-PSDB; ADO00854.
XX
PT Use of compound comprising antibody molecule specific for CD 44, linker
PT moiety and compound toxic to cells, in combination with radiotherapy for
PT preparation of pharmaceutical composition for treatment of cancer.

```
XX
PS   Claim 7; SEQ ID NO 8; 42pp; English.
XX
CC   The present invention describes using a compound (CD) of formula A(LB)n,
CC   where A is an antibody molecule which is specific for CD44, L is a linker
CC   moiety, B is a compound which is toxic to cells, and n is a decimal
CC   number between 1-10, for the preparation of a pharmaceutical composition
CC   for the treatment of cancer, where CD is used or is for use in
CC   combination with radiotherapy. Also described: (1) use of a conjugate
CC   (CJ) of a CD44v6 specific antibody molecule and a maytansinoid for the
CC   manufacture of a pharmaceutical composition for the treatment of cancer,
CC   where CJ is used or is for use in combination with radiotherapy; (2) a
CC   pharmaceutical composition comprising CD or CJ together with a
CC   radioimmunotherapeutic agent and optionally further comprising one or
CC   more carrier(s), diluent(s), or excipient(s); (3) a kit comprising, in a
CC   separate pharmaceutical composition, CD or CJ and a
CC   radioimmunotherapeutic agent; and (4) use of radioimmunotherapeutic agent
CC   (RA) for the preparation of a pharmaceutical composition for the
CC   treatment of cancer, where the radioimmunotherapeutic agent is used or is
CC   for use in combination with CD or CJ. CD and CJ have cytostatic
CC   activities, and can be used as immunostimulators. CJ is useful for the
CC   manufacture of a medicament for the treatment of cancer e.g. head and
CC   neck squamous cell carcinoma, oesophagus squamous cell carcinoma, lung
CC   squamous cell carcinoma, skin squamous cell carcinoma, cervix squamous
CC   cell carcinoma, breast adenocarcinoma, lung adenocarcinoma, pancreas
CC   adenocarcinoma, colon adenocarcinoma, and stomach adenocarcinoma. CD and
CC   CJ are useful for preparation of a pharmaceutical composition for the
CC   treatment of cancer. CD and CJ are useful for treating cancer in a
CC   patient which involves administering CD or CJ to the patient in
CC   combination with radiotherapy. CD and CJ are useful as an adjuvant to
CC   surgical interaction, to treat minimal residual disease. The present
CC   sequence represents a humanised murine antibody BIWA 8 light chain, which
CC   is used in the exemplification of the present invention.
XX
SQ   Sequence 213 AA;

  Query Match             66.4%;  Score 753;  DB 8;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 5.4e-50;
  Matches  156;  Conservative   14;  Mismatches   40;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:| :|    :: ||  |:|:||      ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWLQQKPGQAPRILIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  |  |   ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 15
AAE35326
ID   AAE35326 standard; protein; 213 AA.
XX
AC   AAE35326;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Humanised murine antibody BIWA4 light chain protein.
XX
KW   CD44; cytotoxic drug; therapy; cancer; tumour; minimal residual disease;
KW   antigen; cytostatic; BIWA4 antibody; murine.
XX
OS   Homo sapiens.
XX
PN   EP1258255-A1.
XX
PD   20-NOV-2002.
XX
PF   18-MAY-2001; 2001EP-00112227.
XX
PR   18-MAY-2001; 2001EP-00112227.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
PI   Adolf G,  Heider K,  Patzelt E,  Sproll M;
XX
DR   WPI; 2003-177273/18.
DR   N-PSDB; AAD53976.
XX
PT   New compound useful for treatment of cancer comprises CD44 specific
PT   antibody molecule conjugated to a highly cytotoxic drug, which cleaves
PT   under intracellular conditions.
XX
PS   Claim 7; Page 14; 31pp; English.
XX
CC   The invention relates to a compound comprising CD44 specific antibody
CC   molecule conjugated to a highly cytotoxic drug, which cleaves under
CC   intracellular conditions. The compound is used in pharmaceutical
CC   composition for the treatment of cancer, solid tumours, and as an
CC   adjuvant to surgical intervention to treat minimal residual disease. The
CC   present sequence is humanised murine antibody BIWA4 light chain protein
CC   used in the invention
XX
SQ   Sequence 213 AA;

  Query Match             66.2%;  Score 751;  DB 6;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 7.6e-50;
  Matches  156;  Conservative   13;  Mismatches   41;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:| :|    :: ||  | |:||      ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWYQQKPGQAPRLLIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  |  |   ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213


Search completed: June  7, 2005, 15:54:04
Job time : 115.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:42:01 ; Search time 29.5 Seconds
(without alignments)
551.644 Million cell updates/sec

Title: US-09-671-953B-7
Perfect score: 1134
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	757	66.8	235	3	US-09-423-439-18	Sequence 18, Appl
2	750	66.1	220	3	US-08-952-235-1	Sequence 1, Appli
3	750	66.1	220	4	US-09-669-971-1	Sequence 1, Appli
4	743	65.5	233	4	US-09-472-087-15	Sequence 15, Appl
5	743	65.5	233	4	US-09-472-087-67	Sequence 67, Appl
6	739	65.2	213	3	US-08-397-411-12	Sequence 12, Appl
7	736	64.9	235	4	US-09-011-769A-27	Sequence 27, Appl
8	734	64.7	236	4	US-09-315-926A-79	Sequence 79, Appl
9	732.5	64.6	234	4	US-09-472-087-17	Sequence 17, Appl
10	732.5	64.6	234	4	US-09-472-087-69	Sequence 69, Appl
11	732	64.6	235	4	US-09-472-087-14	Sequence 14, Appl
12	732	64.6	235	4	US-09-472-087-65	Sequence 65, Appl
13	731.5	64.5	224	4	US-09-456-090A-84	Sequence 84, Appl
14	731.5	64.5	224	4	US-09-453-234-84	Sequence 84, Appl
15	730.5	64.4	491	4	US-10-011-125A-2	Sequence 2, Appli
16	728.5	64.2	214	3	US-08-397-411-5	Sequence 5, Appli
17	728	64.2	239	4	US-09-627-896B-22	Sequence 22, Appl
18	726.5	64.1	214	4	US-09-472-087-71	Sequence 71, Appl
19	726.5	64.1	224	4	US-09-456-090A-46	Sequence 46, Appl
20	726.5	64.1	224	4	US-09-453-234-46	Sequence 46, Appl
21	725	63.9	234	4	US-09-740-002-26	Sequence 26, Appl
22	724.5	63.9	234	4	US-09-740-002-24	Sequence 24, Appl
23	724	63.8	214	1	US-08-458-516-12	Sequence 12, Appl
24	724	63.8	235	3	US-09-171-945-17	Sequence 17, Appl
25	722.5	63.7	224	4	US-09-456-090A-36	Sequence 36, Appl
26	722.5	63.7	224	4	US-09-453-234-36	Sequence 36, Appl
27	722.5	63.7	226	4	US-09-456-090A-74	Sequence 74, Appl
28	722.5	63.7	226	4	US-09-453-234-74	Sequence 74, Appl
29	722	63.7	233	3	US-09-485-737B-69	Sequence 69, Appl
30	722	63.7	233	4	US-10-071-485-69	Sequence 69, Appl
31	721.5	63.6	218	5	PCT-US96-13152-2	Sequence 2, Appli
32	721.5	63.6	236	1	US-08-157-101A-5	Sequence 5, Appli
33	720.5	63.5	213	3	US-08-630-820-6	Sequence 6, Appli
34	720.5	63.5	213	4	US-09-273-453-6	Sequence 6, Appli
35	719	63.4	219	3	US-09-027-449-72	Sequence 72, Appl
36	719	63.4	219	3	US-09-026-985-72	Sequence 72, Appl
37	719	63.4	219	4	US-09-121-952A-72	Sequence 72, Appl
38	719	63.4	219	4	US-09-234-340A-72	Sequence 72, Appl
39	719	63.4	235	3	US-09-171-945-97	Sequence 97, Appl
40	719	63.4	242	3	US-09-027-449-56	Sequence 56, Appl
41	719	63.4	242	3	US-08-804-444A-56	Sequence 56, Appl
42	719	63.4	242	3	US-09-026-985-56	Sequence 56, Appl
43	719	63.4	242	4	US-09-121-952A-56	Sequence 56, Appl
44	719	63.4	242	4	US-09-234-340A-56	Sequence 56, Appl
45	718.5	63.4	214	3	US-09-247-352-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-423-439-18
; Sequence 18, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18

Query Match 66.8%; Score 757; DB 3; Length 235;
Best Local Similarity 71.8%; Pred. No. 7.9e-67;
Matches 155; Conservative 15; Mismatches 40; Indels 6; Gaps 3;

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Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |::|  | |: |||| ||:|||:|    ::  | :| |:||       |  |:| | |||
Db         25 VLSQSPAILSASPGEKVTMTCRAS----SSVTYIHWYQQKPGSSPKSWIYATSNLASGVP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |   :|||:  : || | |:|  |      ||||||| :  ||||||||||
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Db         81 ARFSGSGSGSTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 2
US-08-952-235-1
; Sequence 1, Application US/08952235
; Patent No. 6207152
;  GENERAL INFORMATION:
;    APPLICANT:  Schwall, Ralph H.
;    APPLICANT:  Tabor, Kelly H.
;    TITLE OF INVENTION:  Hepatocyte Growth Factor Receptor
;    TITLE OF INVENTION:  Antagonists and Uses Thereof
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/952,235
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/460368
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marschang, Diane L.
;      REGISTRATION NUMBER:  35,600
;      REFERENCE/DOCKET NUMBER:  P0938P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5416
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  220 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-952-235-1

  Query Match             66.1%;  Score 750;  DB 3;  Length 220;
  Best Local Similarity   71.8%;  Pred. No. 3.6e-66;
  Matches  153;  Conservative   13;  Mismatches   43;  Indels    4;  Gaps    2;

Qy          9 SALTTSPGETVTLTCRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAPGVPARF 65
              |:|| | || ||::|:||   : ||   || | |:||       ||   : |  ||| ||
Db          9 SSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRF 68

Qy         66 SGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
              :||  |    ||||  : :| | |:|  :|   | ||||||| :  |||||||||||||
Db         69 TGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEI-KRTVAAPSVFIFPPS 127

Qy        126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 187

Qy        186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        188 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220


RESULT 3
US-09-669-971-1
; Sequence 1, Application US/09669971
; Patent No. 6468529
;  GENERAL INFORMATION:
;       APPLICANT: Schwall, Ralph H.
;                  Tabor, Kelly H.
;       TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
;                           Antagonists and Uses Thereof
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/669,971
;            FILING DATE: 05-Jul-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/952,235
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/460368
;            FILING DATE: 02-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Marschang, Diane L.
;            REGISTRATION NUMBER: 35,600
;            REFERENCE/DOCKET NUMBER: P0938P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-5416
;            TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 220 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-669-971-1

  Query Match             66.1%;  Score 750;  DB 4;  Length 220;
  Best Local Similarity   71.8%;  Pred. No. 3.6e-66;
  Matches  153;  Conservative   13;  Mismatches   43;  Indels    4;  Gaps    2;

Qy          9 SALTTSPGETVTLTCRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAPGVPARF 65
              |:|| | || ||::|:||   : ||   || | |:||       ||   : |  ||| ||
Db          9 SSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRF 68

Qy         66 SGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
              :||  |    ||||  : :| | |:|  :|   | ||||||| :  |||||||||||||
Db         69 TGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEI-KRTVAAPSVFIFPPS 127

Qy        126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
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Db        128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 187

Qy        186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db        188 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220


RESULT 4
US-09-472-087-15
; Sequence 15, Application US/09472087
; Patent No. 6682736
```

```
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-15

  Query Match             65.5%;  Score 743;  DB 4;  Length 233;
  Best Local Similarity   70.4%;  Pred. No. 1.9e-65;
  Matches  152;  Conservative   19;  Mismatches   39;  Indels    6;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||  ||:||:|:    :|:|  | |:||       || | ::|| |:|
Db         23 VLTQSPGTLSLSPGERATLSCRTSV----SSSYLAWYQQKPGQAPRLLIYGASSRATGIP 78

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
               |||||  |    |||:  : || | |:|  :  : : ||||||: :  ||||||||||
Db         79 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGISPFTFGGGTKVEI-KRTVAAPSVFIF 137

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 197

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db        198 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 233


RESULT 5
US-09-472-087-67
; Sequence 67, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-67

  Query Match             65.5%;  Score 743;  DB 4;  Length 233;
  Best Local Similarity   70.4%;  Pred. No. 1.9e-65;
  Matches  152;  Conservative   19;  Mismatches   39;  Indels    6;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||  ||:||:|:    :|:|  | |:||       || | ::|| |:|
Db         23 VLTQSPGTLSLSPGERATLSCRTSV----SSSYLAWYQQKPGQAPRLLIYGASSRATGIP 78

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
               |||||  |    |||:  : || | |:|  :  : : ||||||: :  ||||||||||
Db         79 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGISPFTFGGGTKVEI-KRTVAAPSVFIF 137

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 197

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        198 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 233


RESULT 6
US-08-397-411-12
; Sequence 12, Application US/08397411
; Patent No. 6129914
;  GENERAL INFORMATION:
;    APPLICANT:  Weiner, George
;    APPLICANT:  Gingrich, Roger
;    APPLICANT:  Link, Brian
;    APPLICANT:  Tso, J. Yun
;    TITLE OF INVENTION:  Bispecific Antibody Effective to Treat
;    TITLE OF INVENTION:  B-Cell Lymphoma and Cell Line
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/397,411
;      FILING DATE:  01-MAR-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/859,583
;      FILING DATE:  27-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  011823-004901
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  213 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-397-411-12

  Query Match             65.2%;  Score 739;  DB 3;  Length 213;
  Best Local Similarity   70.7%;  Pred. No. 4.2e-65;
  Matches  152;  Conservative   16;  Mismatches   41;  Indels    6;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  |:|: | |: ||:|| :|    :: :| || |:||       ||  |:  | |||:
Db          4 MTQSPSSLSASVGDRVTITCSAS----SSVSYMNWYQQKPGKAPKRLIYDTSKLASGVPS 59

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
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Db         60 RFSGSGSGTDFTLTISSLQPEDFDTYYCQQWSSNPPTFGGGTKVEI-KRTVAAPSVFIFP 118

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 178

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        179 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213


RESULT 7
US-09-011-769A-27
; Sequence 27, Application US/09011769A
; Patent No. 6436691
;   GENERAL INFORMATION:
;        APPLICANT: SLATER, Anthony M.
;                   BLAKEY, David C.
;                   DAVIES, David H.
;                   HENNAM, John F.
;                   HENNEQUIN, Laurent F.A.
;                   MARSHAM, Peter R.
;                   DOWELL, Robert I.
;        TITLE OF INVENTION: Chemical Compounds
;        NUMBER OF SEQUENCES: 87
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Madison & Sutro, LLP
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 1.44 Mb disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/011,769A
;             FILING DATE: 13-Feb-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB96/01975
;             FILING DATE: 13-AUG-1996
;             APPLICATION NUMBER: GB 9612295.7
;             FILING DATE: 12-JUN-1996
;             APPLICATION NUMBER: GB 9611019.2
;             FILING DATE: 25-MAY-1996
;             APPLICATION NUMBER: GB 9516810.0
;             FILING DATE: 16-AUG-1995
;   INFORMATION FOR SEQ ID NO: 27:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 235 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-011-769A-27

  Query Match             64.9%;  Score 736;  DB 4;  Length 235;
  Best Local Similarity   70.8%;  Pred. No. 9.4e-65;
  Matches  153;  Conservative   15;  Mismatches   42;  Indels    6;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  |:|: | |: ||:|||:|    ::  | :| |:||       |  |:| | |||
Db         25 VLTQSPSSLSVSVGDRVTMTCRAS----SSVTYIHWYQQKPGLAPKSWIYATSNLASGVP 80

Qy         63 ARFSGSGLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              :|||||  |    |||:  | || | |:|  |      || |||: |  ||||||||||
Db         81 SRFSGSGSGTDYTLTISSLQPEDIATYYCQHWSSKPPTFGQGTKVEV-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 8
US-09-315-926A-79
; Sequence 79, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
;  APPLICANT: Es van, Helmuth
;  APPLICANT:  Havenga, Menzo
;  APPLICANT:  Verlinden, Stefan
;  TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
;  FILE REFERENCE: 2183-4080US
;  CURRENT APPLICATION NUMBER: US/09/315,926A
;  CURRENT FILING DATE:  1999-05-20
;  PRIOR APPLICATION NUMBER: EP 99201593.3
;  PRIOR FILING DATE: 1999-05-20
;  PRIOR APPLICATION NUMBER: EP 98201693.3
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Description of Artificial Sequence: phage
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(236)
;   OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-79

  Query Match             64.7%;  Score 734;  DB 4;  Length 236;
  Best Local Similarity   72.6%;  Pred. No. 1.5e-64;
  Matches  151;  Conservative   14;  Mismatches   41;  Indels    2;  Gaps    2;

Qy         11 LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPARFSGSLI 70
              |: |||   ||:||:|  :|:: | | | |:||      || | :||| ||| |||||
Db         31 LSLSPGAGATLSCRAS-QSVSSSRNLA-WYQQKPGQAPRLLIYGVSNRATGVPDRFSGSGS 88

Qy         71 GDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPSDEQLK 130
              |    |||   : || | |:|  :  :|| || |||: :   ||||||||||||||||||
Db         89 GADFTLTINRLEPEDFAVYYCQRYGRSLWTFGQGTKVEIKRGTVAAPSVFIFPPSDEQLK 148

Qy        131 SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY 208

Qy        191 EKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||| ||||||||||
Db        209 EKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 9
US-09-472-087-17
; Sequence 17, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
```

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;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-17

  Query Match             64.6%;  Score 732.5;  DB 4;  Length 234;
  Best Local Similarity   69.9%;  Pred. No. 2.1e-64;
  Matches  151;  Conservative   18;  Mismatches   42;  Indels    5;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: |||| ||:||:|    : |:|  | |:||      || | ::|| |:|
Db         23 VLTQSPGTLSLSPGERATLSCRAS---QSVSSYLAWYQQKPGQAPRPLIYGVSSRATGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
               ||||| |    |||:  : || | |:|  :  : : || |||: :  ||||||||||
Db         80 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGISPFTFGPGTKVDI-KRTVAAPSVFIF 138

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 10
US-09-472-087-69
; Sequence 69, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-69

  Query Match             64.6%;  Score 732.5;  DB 4;  Length 234;
  Best Local Similarity   69.9%;  Pred. No. 2.1e-64;
  Matches  151;  Conservative   18;  Mismatches   42;  Indels    5;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: |||| ||:||:|    : |:|  | |:||      || | ::|| |:|
Db         23 VLTQSPGTLSLSPGERATLSCRAS---QSVSSYLAWYQQKPGQAPRPLIYGVSSRATGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
               ||||| |    |||:  : || | |:|  :  : : || |||: :  ||||||||||
Db         80 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGISPFTFGPGTKVDI-KRTVAAPSVFIF 138

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 11
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-14

  Query Match             64.6%;  Score 732;  DB 4;  Length 235;
  Best Local Similarity   69.4%;  Pred. No. 2.3e-64;
  Matches  150;  Conservative   19;  Mismatches   43;  Indels    4;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: |||| ||:||:|     :|::  | |::|      || | ::|| |:|
Db         23 VLTQSPGTLSLSPGERATLSCRAS--QSISSSFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
               ||||| |    |||:  : || | |:|  :  : | || |||: :  ||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPWTFGQGTKVEI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 12
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-65

  Query Match             64.6%;  Score 732;  DB 4;  Length 235;
  Best Local Similarity   69.4%;  Pred. No. 2.3e-64;
  Matches  150;  Conservative   19;  Mismatches   43;  Indels    4;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||  ||:||:|     :|::  | |::|       || | ::|| |:|
Db         23 VLTQSPGTLSLSPGERATLSCRAS--QSISSSFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
               |||||  |    |||:  : || | |:|  :  : | || |||: :  ||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPWTFGQGTKVEI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 13
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-32L
US-09-456-090A-84

  Query Match             64.5%;  Score 731.5;  DB 4;  Length 224;
  Best Local Similarity   71.4%;  Pred. No. 2.5e-64;
  Matches  155;  Conservative   14;  Mismatches   39;  Indels    9;  Gaps    5;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
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Db          3 VLTQSPATLSLSPGERATLSCRAS---QSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIP 59

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLW--VFGGGTKLTVLSRTVAAPSVF 120
              ||||||  |    |||:  : || | |:|     | |   ||||||: :  |||||||||
Db         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQ--QRNNWPLTFGGGTKVEI-KRTVAAPSVF 116

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 176

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGE 217
              |||||||||||||||||||||| ||||||||||
Db        177 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213


RESULT 14
US-09-453-234-84
; Sequence 84, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-32L
US-09-453-234-84

  Query Match             64.5%;  Score 731.5;  DB 4;  Length 224;
  Best Local Similarity   71.4%;  Pred. No. 2.5e-64;
  Matches  155;  Conservative   14;  Mismatches   39;  Indels    9;  Gaps    5;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:||:|     : |:|  | |:||      ||   :||| |:|
Db          3 VLTQSPATLSLSPGERATLSCRAS---QSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIP 59

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLW--VFGGGTKLTVLSRTVAAPSVF 120
              ||||||  |    |||:  : || | |:|     | |   ||||||: :  |||||||||
Db         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQ--QRNNWPLTFGGGTKVEI-KRTVAAPSVF 116

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 176

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGE 217
              |||||||||||||||||||||| ||||||||||
Db        177 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 213


RESULT 15
US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
;  APPLICANT: Chen, Christina Yu-Ching
;  TITLE OF INVENTION: BACTERIAL HOST STRAINS
;  FILE REFERENCE: P1804R1
;  CURRENT APPLICATION NUMBER: US/10/011,125A
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: US 60/256,162
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2

  Query Match             64.4%;  Score 730.5;  DB 4;  Length 491;
  Best Local Similarity   70.7%;  Pred. No. 8.8e-64;
  Matches  152;  Conservative   15;  Mismatches   43;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  |:|: | |: ||:|| :|      ||| || |:||      ||  |::   |||:
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Db         27 LTQSPSSLSASVGDRVTITCSAS---QDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 83

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  |    |||:  | || | |:|  :    | || |||: :  ||||||||||||
Db         84 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEI-KRTVAAPSVFIFP 142

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 202

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        203 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
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Job time : 30.5 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 16:00:22 ; Search time 100 Seconds
(without alignments)
785.243 Million cell updates/sec

Title: US-09-671-953B-7
Perfect score: 1134
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published_Applications_AA:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1083	95.5	218	16	US-10-625-047-27	Sequence 27, Appl
2	1082	95.4	218	16	US-10-625-047-28	Sequence 28, Appl
3	759.5	67.0	235	16	US-10-723-003-42	Sequence 42, Appl
4	753	66.4	213	14	US-10-150-475A-8	Sequence 8, Appli
5	753	66.4	213	16	US-10-704-522-8	Sequence 8, Appli
6	753	66.4	213	16	US-10-645-215-8	Sequence 8, Appli
7	751	66.2	213	14	US-10-150-475A-4	Sequence 4, Appli
8	751	66.2	213	16	US-10-704-522-4	Sequence 4, Appli
9	751	66.2	213	16	US-10-645-215-4	Sequence 4, Appli
10	750	66.1	220	9	US-09-995-693-1	Sequence 1, Appli
11	750	66.1	220	14	US-10-232-408-1	Sequence 1, Appli
12	745	65.7	213	15	US-10-435-299-12	Sequence 12, Appl
13	743.5	65.6	234	10	US-09-848-832-4	Sequence 4, Appli
14	743.5	65.6	234	14	US-10-225-108A-4	Sequence 4, Appli
15	743.5	65.6	234	15	US-10-461-148-2	Sequence 2, Appli
16	743	65.5	233	14	US-10-153-382-11	Sequence 11, Appl
17	743	65.5	233	16	US-10-612-497-15	Sequence 15, Appl
18	743	65.5	233	16	US-10-612-497-67	Sequence 67, Appl
19	743	65.5	233	16	US-10-776-649-15	Sequence 15, Appl
20	743	65.5	233	16	US-10-776-649-67	Sequence 67, Appl
21	739.5	65.2	234	15	US-10-045-674-587	Sequence 587, App
22	739	65.2	215	15	US-10-307-724-122	Sequence 122, App
23	739	65.2	215	16	US-10-737-290-122	Sequence 122, App
24	739	65.2	239	16	US-10-737-290-142	Sequence 142, App
25	738	65.1	213	15	US-10-474-832-3	Sequence 3, Appli
26	738	65.1	213	16	US-10-818-765-3	Sequence 3, Appli
27	735	64.8	215	16	US-10-128-520-106	Sequence 106, App
28	735	64.8	235	15	US-10-656-769-38	Sequence 38, Appl
29	734	64.7	236	14	US-10-235-175-79	Sequence 79, Appl
30	734	64.7	669	9	US-09-807-721-2	Sequence 2, Appli
31	733.5	64.7	234	15	US-10-292-088-88	Sequence 88, Appl
32	732.5	64.6	234	14	US-10-153-382-15	Sequence 15, Appl
33	732.5	64.6	234	16	US-10-612-497-17	Sequence 17, Appl
34	732.5	64.6	234	16	US-10-612-497-69	Sequence 69, Appl
35	732.5	64.6	234	16	US-10-776-649-17	Sequence 17, Appl
36	732.5	64.6	234	16	US-10-776-649-69	Sequence 69, Appl
37	732	64.6	215	15	US-10-408-901-40	Sequence 40, Appl
38	732	64.6	215	15	US-10-408-901-48	Sequence 48, Appl
39	732	64.6	215	15	US-10-408-901-52	Sequence 52, Appl
40	732	64.6	215	16	US-10-128-520-129	Sequence 129, App
41	732	64.6	235	14	US-10-153-382-7	Sequence 7, Appli
42	732	64.6	235	16	US-10-612-497-14	Sequence 14, Appl
43	732	64.6	235	16	US-10-612-497-65	Sequence 65, Appl
44	732	64.6	235	16	US-10-776-649-14	Sequence 14, Appl
45	732	64.6	235	16	US-10-776-649-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-10-625-047-27
; Sequence 27, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Corneillie, Todd
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 02307O-130910US
; CURRENT APPLICATION NUMBER: US/10/625,047
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:native cloned
; OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region
; OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody
; OTHER INFORMATION: kappa light chain constant region (TTCL)
US-10-625-047-27

Query Match 95.5%; Score 1083; DB 16; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.1e-84;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
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Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

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Db        181 STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218


RESULT 2
US-10-625-047-28
; Sequence 28, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
;  APPLICANT: Meares, Claude
;  APPLICANT:  Corneillie, Todd
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Multi-Functional Antibodies
;  FILE REFERENCE: 02307O-130910US
;  CURRENT APPLICATION NUMBER: US/10/625,047
;  CURRENT FILING DATE:  2003-07-22
;  PRIOR APPLICATION NUMBER: US 10/350,555
;  PRIOR FILING DATE: 2003-01-23
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:N53C cloned
;   OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable
;   OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin
;   OTHER INFORMATION: antibody kappa light chain constant region (TTCL)
US-10-625-047-28

  Query Match             95.4%;  Score 1082;  DB 16;  Length 218;
  Best Local Similarity   95.9%;  Pred. No. 1.3e-84;
  Matches  209;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
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Db          1 RSAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGCNNRPPG 60

Qy         61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
              |||||||||||||||||| | |||||| ||||||| | ||||||||||||||||||||||
Db         61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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Db        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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RESULT 3
US-10-723-003-42
; Sequence 42, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
;  APPLICANT: MA, Jing
;  APPLICANT:  GUO, Yajun
;  TITLE OF INVENTION: PREPARATION AND APPLICATION OF
;  TITLE OF INVENTION:  ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
;  FILE REFERENCE: 549062000200
;  CURRENT APPLICATION NUMBER: US/10/723,003
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: CN 2003101199300
;  PRIOR FILING DATE: 2003-11-25
;  PRIOR APPLICATION NUMBER: CN 031292909
;  PRIOR FILING DATE: 2003-06-13
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-723-003-42

  Query Match             67.0%;  Score 759.5;  DB 16;  Length 235;
  Best Local Similarity   70.5%;  Pred. No. 5.8e-57;
  Matches  155;  Conservative   16;  Mismatches   42;  Indels    7;  Gaps    3;

Qy          1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              | .:|  :|   |: |||| ||:|||:|    :: :| :| |:||       |  |:| |
Db         21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLA 76

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS 118
               ||| |||||  |   :|||:  : || | |:|  |  |   ||||||| :  |||||||
Db         77 SGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEI-KRTVAAPS 135

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
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Db        136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db        196 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 4
US-10-150-475A-8
; Sequence 8, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, G. et al.
;  TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1211
;  CURRENT APPLICATION NUMBER: US/10/150,475A
;  CURRENT FILING DATE:  2002-05-17
;  PRIOR APPLICATION NUMBER: US 60/307,451
;  PRIOR FILING DATE: 2001-07-24
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Humanised
;   OTHER INFORMATION: Murine Antibody BIWA 8 Light Chain SEQ ID NO: 8
US-10-150-475A-8

  Query Match             66.4%;  Score 753;  DB 14;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 1.9e-56;
  Matches  156;  Conservative   14;  Mismatches   40;  Indels    6;  Gaps    3;

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Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
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Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177
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Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
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RESULT 5
US-10-704-522-8
; Sequence 8, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baumann, Michael
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and methods for treating cancer using
; TITLE OF INVENTION: cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1414
; CURRENT APPLICATION NUMBER: US/10/704,522
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/429,516
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP 02024881
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 8 Light Chain
US-10-704-522-8

Query Match 66.4%; Score 753; DB 16; Length 213;
Best Local Similarity 72.2%; Pred. No. 1.9e-56;
Matches 156; Conservative 14; Mismatches 40; Indels 6; Gaps 3;

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Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
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Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWLQQKPGQAPRILIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
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Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
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RESULT 6
US-10-645-215-8
; Sequence 8, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/10/645,215
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Antibody BIWA 8 Light Chain
US-10-645-215-8

Query Match 66.4%; Score 753; DB 16; Length 213;
Best Local Similarity 72.2%; Pred. No. 1.9e-56;
Matches 156; Conservative 14; Mismatches 40; Indels 6; Gaps 3;

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Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
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Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWLQQKPGQAPRILIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  |  |   ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
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RESULT 7
US-10-150-475A-4
; Sequence 4, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Light Chain SEQ ID NO: 4
US-10-150-475A-4

Query Match 66.2%; Score 751; DB 14; Length 213;
Best Local Similarity 72.2%; Pred. No. 2.8e-56;
Matches 156; Conservative 13; Mismatches 41; Indels 6; Gaps 3;

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Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
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Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWYQQKPGQAPRLLIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
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Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
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RESULT 8
US-10-704-522-4
; Sequence 4, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, Gunther
;  APPLICANT:  Baumann, Michael
;  APPLICANT:  Heider, Karl-Heinz
;  TITLE OF INVENTION: Compositions and methods for treating cancer using
;  TITLE OF INVENTION:  cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1414
;  CURRENT APPLICATION NUMBER: US/10/704,522
;  CURRENT FILING DATE:  2003-11-07
;  PRIOR APPLICATION NUMBER: US 60/429,516
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: EP 02024881
;  PRIOR FILING DATE: 2002-11-08
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-10-704-522-4

  Query Match             66.2%;  Score 751;  DB 16;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 2.8e-56;
  Matches  156;  Conservative   13;  Mismatches   41;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:| :|    :: ||  | |:||       ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWYQQKPGQAPRLLIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  |  |   ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213


RESULT 9
US-10-645-215-4
; Sequence 4, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, Guenther
;  APPLICANT:  Baum, Anke
;  APPLICANT:  Heider, Karl-Heinz
;  TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
;  TITLE OF INVENTION:  Cytotoxic CD44 Antibody Immunoconjugates and
;  TITLE OF INVENTION:  Chemotherapeutic Agents
;  FILE REFERENCE: 1/1383
;  CURRENT APPLICATION NUMBER: US/10/645,215
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: EP 02 018 686.2
;  PRIOR FILING DATE: August 21, 2002
;  PRIOR APPLICATION NUMBER: US 60/405,956
;  PRIOR FILING DATE: August 26, 2002
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-10-645-215-4

  Query Match             66.2%;  Score 751;  DB 16;  Length 213;
  Best Local Similarity   72.2%;  Pred. No. 2.8e-56;
  Matches  156;  Conservative   13;  Mismatches   41;  Indels    6;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:| :|    :: ||  | |:||       ||  |:| | |||
Db          3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWYQQKPGQAPRLLIYLTSNLASGVP 58

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |||:  : || | |:|  |  |   ||||||: :  ||||||||||
Db         59 ARFSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213


RESULT 10
US-09-995-693-1
; Sequence 1, Application US/09995693
; Patent No. US20020136721A1
;  GENERAL INFORMATION:
;       APPLICANT: Schwall, Ralph H.
;                  Tabor, Kelly H.
;       TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
;                           Antagonists and Uses Thereof
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/995,693
;            FILING DATE: 29-No. US20020136721A1-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/952,235
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Marschang, Diane L.
;            REGISTRATION NUMBER: 35,600
;            REFERENCE/DOCKET NUMBER: P0938P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-5416
;            TELEFAX: 650/952-9881
;  INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 220 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-995-693-1

  Query Match             66.1%;  Score 750;  DB 9;  Length 220;
  Best Local Similarity   71.8%;  Pred. No. 3.5e-56;
  Matches  153;  Conservative   13;  Mismatches   43;  Indels    4;  Gaps    2;
```

```
Qy          9 SALTTSPGETVTLTCRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAPGVPARF 65
              |:|| | || ||::|:||   : ||   ||  | |:||      ||   : |  ||| ||
Db          9 SSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRF 68

Qy         66 SGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
              :||  |    |||| : :| | |:|  :|   | ||||||| :  ||||||||||||||
Db         69 TGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEI-KRTVAAPSVFIFPPS 127

Qy        126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 187

Qy        186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||| ||||||||||
Db        188 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
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RESULT 11
US-10-232-408-1
; Sequence 1, Application US/10232408
; Publication No. US20030118587A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,408
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/669,971
; FILING DATE: 05-Jul-2001
; APPLICATION NUMBER: US/08/952,235
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/460368
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-232-408-1

Query Match 66.1%; Score 750; DB 14; Length 220;
Best Local Similarity 71.8%; Pred. No. 3.5e-56;
Matches 153; Conservative 13; Mismatches 43; Indels 4; Gaps 2;

```
Qy          9 SALTTSPGETVTLTCRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAPGVPARF 65
              |:|| | || ||::|:||   : ||   ||  | |:||      ||   : |  ||| ||
Db          9 SSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRF 68

Qy         66 SGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
              :||  |    |||| : :| | |:|  :|   | ||||||| :  ||||||||||||||
Db         69 TGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLEI-KRTVAAPSVFIFPPS 127

Qy        126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 187

Qy        186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||| ||||||||||
Db        188 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
```

RESULT 12
US-10-435-299-12
; Sequence 12, Application US/10435299
; Publication No. US20040052783A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3
; FILE REFERENCE: 05882-0176-CNUS04
; CURRENT APPLICATION NUMBER: US/10/435,299
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 09/618,380
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 08/397,411
; PRIOR FILING DATE: 1995-03-01
; PRIOR APPLICATION NUMBER: US 07/859,583
; PRIOR FILING DATE: 1992-03-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Complete light chain of Humanized M291 Ab
US-10-435-299-12

Query Match 65.7%; Score 745; DB 15; Length 213;
Best Local Similarity 71.2%; Pred. No. 9.1e-56;
Matches 153; Conservative 16; Mismatches 40; Indels 6; Gaps 3;

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Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :+|  |:|: | |: ||:|| :|    :: :| || |:||      ||  |:  | |||:
Db          4 MTQSPSSLSASVGDRVTITCSAS----SSVSYMNWYQQKPGKAPKRLIYDTSKLASGVPS 59

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  |    |||:  | || | |:|  |  |   ||||||: :  ||||||||||
Db         60 RFSGSGSGTDFTLTISSLQPEDFATYYCQQWSSNPPTFGGGTKVEI-KRTVAAPSVFIFP 118

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 178

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||| ||||||||||
Db        179 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
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RESULT 13
US-09-848-832-4
; Sequence 4, Application US/09848832
; Publication No. US20030165507A1
; GENERAL INFORMATION:
; APPLICANT: Hooper, Douglas
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RABIES VIRUS-SPECFIC NEUTRALIZING HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
; FILE REFERENCE: HOO01.NP0002

```
;  CURRENT APPLICATION NUMBER: US/09/848,832
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: 60/204,518
;  PRIOR FILING DATE: 2000-05-16
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-848-832-4

  Query Match             65.6%;  Score 743.5;  DB 10;  Length 234;
  Best Local Similarity   71.8%;  Pred. No. 1.4e-55;
  Matches  155;  Conservative   12;  Mismatches   44;  Indels    5;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  || ||:|    | | |  | |:||      ||  |:||| |:|
Db         23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |:|:  : || | |:|   :   | || |||:    ||||||||||
Db         80 ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF 138

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||| ||||||||||
Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 14
US-10-225-108A-4
; Sequence 4, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
;  APPLICANT: HOOPER, Craig
;  APPLICANT:  DIETZSCHOLD, Bernhard
;  TITLE OF INVENTION: Recombinant Antibodies, and Compositions
;  TITLE OF INVENTION:  and Methods for Making Them
;  FILE REFERENCE: 8321-110
;  CURRENT APPLICATION NUMBER: US/10/225,108A
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: US 09/848,832
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/204,518
;  PRIOR FILING DATE: 2001-05-16
;  PRIOR APPLICATION NUMBER: US 60/314,023
;  PRIOR FILING DATE: 2001-08-21
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-225-108A-4

  Query Match             65.6%;  Score 743.5;  DB 14;  Length 234;
  Best Local Similarity   71.8%;  Pred. No. 1.4e-55;
  Matches  155;  Conservative   12;  Mismatches   44;  Indels    5;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  || ||:|    | | |  | |:||      ||  |:||| |:|
Db         23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |:|:  : || | |:|   :   | || |||:    ||||||||||
Db         80 ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF 138

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||| ||||||||||
Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 15
US-10-461-148-2
; Sequence 2, Application US/10461148
; Publication No. US20040013672A1
; GENERAL INFORMATION:
;  APPLICANT: Dietzschold, Bernhard
;  APPLICANT:  Hooper, Douglas C.
;  TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
;  TITLE OF INVENTION:  AND METHODS FOR MAKING AND USING THE SAME
;  FILE REFERENCE: 8321-110CI1-185685
;  CURRENT APPLICATION NUMBER: US/10/461,148
;  CURRENT FILING DATE:  2003-06-13
;  PRIOR APPLICATION NUMBER: US 10/225,108
;  PRIOR FILING DATE: 2002-08-21
;  PRIOR APPLICATION NUMBER: US 60/314,023
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 09/848,832
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/204,518
;  PRIOR FILING DATE: 2000-05-16
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Human
US-10-461-148-2

  Query Match             65.6%;  Score 743.5;  DB 15;  Length 234;
  Best Local Similarity   71.8%;  Pred. No. 1.4e-55;
  Matches  155;  Conservative   12;  Mismatches   44;  Indels    5;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  || ||:|    | | |  | |:||      ||  |:||| |:|
Db         23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              ||||||  |    |:|:  : || | |:|   :   | || |||:    ||||||||||
Db         80 ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF 138

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||| ||||||||||
Db        199 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


Search completed: June  7, 2005, 16:18:38
Job time : 100 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:39:10 ; Search time 25 Seconds
(without alignments)
839.010 Million cell updates/sec

Title: US-09-671-953B-7
Perfect score: 1134
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	739	65.2	215	2	JE0242	Ig kappa chain NIG
2	735	64.8	215	2	JE0244	Ig kappa chain NIG
3	728.5	64.2	214	2	PC4156	Ig lambda chain V
4	721	63.6	215	2	JE0243	Ig kappa chain NIG
5	678.5	59.8	216	2	JE0241	Ig kappa chain Am3
6	672	59.3	215	2	A23746	Ig kappa chain V-I
7	578.5	51.0	135	2	S52059	JC-kappa protein -
8	549.5	48.5	240	2	S06084	Ig kappa chain pre
9	547.5	48.3	287	4	PC4402	pelB leader/Ig hea
10	544	48.0	106	1	K3HU	Ig kappa chain C r
11	541	47.7	128	2	S52450	Ig lambda chain V
12	534.5	47.1	220	2	A31790	Ig kappa chain V r
13	533	47.0	129	1	L1MS4E	Ig lambda-1 chain
14	526	46.4	235	2	S25058	Ig kappa chain - m
15	525	46.3	113	2	S06819	Ig lambda chain V
16	523.5	46.2	112	2	S06818	Ig lambda chain V
17	521	45.9	106	2	S20654	Ig lambda chain V
18	513.5	45.3	114	2	S06820	Ig lambda chain V
19	511	45.1	219	2	S38865	Ig kappa chain - m
20	511	45.1	225	2	S37484	Ig kappa chain - m
21	509	44.9	99	2	A37927	Ig kappa chain C r
22	504.5	44.5	234	2	S14237	Ig kappa chain pre
23	503	44.4	99	2	S26653	Ig kappa chain C r
24	502.5	44.3	230	2	S33161	Ig kappa chain - s
25	500	44.1	113	2	B54256	Ig lambda-1 chain
26	499.5	44.0	114	2	S06822	Ig lambda chain V
27	498	43.9	129	1	L2MS35	Ig lambda-2 chain
28	497.5	43.9	214	2	S68212	Ig kappa chain (Ma
29	497.5	43.9	218	2	S68241	Ig kappa chain V r
30	495.5	43.7	225	2	JL0029	Ig kappa chain pre
31	495.5	43.7	234	2	S01320	Ig kappa chain pre
32	492.5	43.4	218	2	JC5810	monoclonal antibod
33	490	43.2	217	2	S42772	Ig kappa chain - m
34	488.5	43.1	99	2	PH1089	Ig lambda chain V
35	488	43.0	219	2	S16112	Ig kappa chain V r
36	486	42.9	99	2	S14582	Ig lambda chain V
37	486	42.9	113	2	S06821	Ig lambda chain V
38	485	42.8	235	2	S25749	Ig lambda chain -
39	484.5	42.7	219	2	PC4203	Ig kappa chain (mo
40	478	42.2	97	2	PH1090	Ig lambda chain V
41	478	42.2	116	1	L1MSV	Ig lambda-1 chain
42	478	42.2	219	2	S52028	Ig kappa chain - m
43	473	41.7	99	2	S14584	Ig lambda chain V
44	473	41.7	100	2	PH1088	Ig lambda chain V
45	469.5	41.4	210	2	A56169	Ig kappa chain V r

ALIGNMENTS

RESULT 1
JE0242
Ig kappa chain NIG26 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda,
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 739; DB 2; Length 215;
Best Local Similarity 70.4%; Pred. No. 1.4e-48;
Matches 152; Conservative 17; Mismatches 43; Indels 4; Gaps 3;

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Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||  ||:||:|     ::||  | |:||    : ||   ::|| |:|
Db          3 VLTQSPGTLSLSPGERATLSCRAS--QSVSNNYLAWYQQKPGQAPSLLIYDASSRATGIP 60

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              |||||  |    |||:| : || | |:|  :    | || |||: :  ||||||||||
Db         61 DRFSGSGSGTDFILTISGLEPEDFAVYYCQQYDRPPWTFGQGTKVEI-KRTVAAPSVFIF 119

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 2
JE0244
Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL am
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

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  Query Match             64.8%;  Score 735;  DB 2;  Length 215;
  Best Local Similarity   71.7%;  Pred. No. 2.9e-48;
  Matches  157;  Conservative   13;  Mismatches   39;  Indels   10;  Gaps    6;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:||:|      || | | |:||      ||   : || |:|
Db          3 VLTQSPATLSVSPGERATLSCRAS--QSVHSNLA-WYQQKPGQAPRLLIYRASTRATGIP 59

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLW---VFGGGTKLTVLSRTVAAPSV 119
              ||||||  |    |||:  |:|| | |:|  :  | |    ||||||: :  ||||||||
Db         60 ARFSGSGSGTDFILTISSLQSEDFALYYCQQY--NTWPPLTFGGGTKVEI-KRTVAAPSV 116

Qy        120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176

Qy        180 SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||| ||||||||||
Db        177 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215


RESULT 3
PC4156
Ig lambda chain V region MabB23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C;Accession: PC4156
R;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 169, 237-239, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mo
A;Reference number: PC4155; MUID:96194809; PMID:8647454
A;Accession: PC4156
A;Molecule type: mRNA
A;Residues: 1-214 <KWA>
A;Cross-references: GB:U28967; NID:g1262178; PIDN:AAC52488.1; PID:g1262179
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-214/Product: light chain #status predicted <MAT>
F;98-110/Region: V region
F;130-198/Domain: immunoglobulin homology <IMM>

  Query Match             64.2%;  Score 728.5;  DB 2;  Length 214;
  Best Local Similarity   66.5%;  Pred. No. 8.8e-48;
  Matches  145;  Conservative   23;  Mismatches   43;  Indels    7;  Gaps    3;

Qy          3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |||||||||||||||||||||: |||||||||:||||||||||||||||||| ||||
Db          2 AVVTQESALTTSPGETVTLTCRSNTGAVTTSNYASWVQEKPDHLFTGLIGGTNNRVPGVP 61

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              |||||||||||||||||||||||| ||||||  | |||||||||||| :  ::||| :|
Db         62 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWNSNHWVFGGGTKLTVLGQPKSSPSVTLF 121

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST--YSLS 180
              ||| |:|::  |::|| : :|||     | ||||    :  :|    | | || |    |  |
Db        122 PPSSEELETNKATLVCTITDFYPGVVTVDWKVDG---TPVTQGMETTQPSKQSNNKYMAS 178

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              | |||:   :|:|  |:|:|||:|     | || :| :|
Db        179 SYLTLTARAWERHSSYSCQVTHEG--HTVEKSLSRADC 214


RESULT 4
JE0243
Ig kappa chain NIG93 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0243
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0243
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             63.6%;  Score 721;  DB 2;  Length 215;
  Best Local Similarity   70.2%;  Pred. No. 3.2e-47;
  Matches  153;  Conservative   12;  Mismatches   45;  Indels    8;  Gaps    4;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:||:|      |       |  :|        ||   : || |||
Db          3 VMTQSPATLSVSPGERATLSCRASQSVATN---VVWYMQKLGQAPRLLIYDASTRATGVP 59

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLW--VFGGGTKLTVLSRTVAAPSVF 120
              ||||||  | :  |||:  |:|| | |:|   : | |   || |||:    |||||||||
Db         60 ARFSGSGSGTEFTLTISSLQSEDFAIYYCQ--HNNAWPPTFGQGTKVETKRRTVAAPSVF 117

Qy        121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 177

Qy        181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||| ||||||||||
Db        178 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215


RESULT 5
JE0241
Ig kappa chain Am37 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0241
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0241
A;Molecule type: protein
A;Residues: 1-216 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>

  Query Match             59.8%;  Score 678.5;  DB 2;  Length 216;
  Best Local Similarity   66.4%;  Pred. No. 5e-44;
  Matches  144;  Conservative   14;  Mismatches   54;  Indels    5;  Gaps    4;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTS-NYANWVQEKPDHLFTGLIGGTNNRAPGV 61
              |:||   |  | ||  |: |:||   :  | |:  | |:||      |:   | |  ||
Db          3 VLTQSPDFLAVSLGERATINCKSSQSVLYNSKNFLAWYQQKPGQ--PKLLIWANVRESGV 60

Qy         62 PARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFI 121
              | || || :|    |||:  | |  | |:|  :|   : || | :| :  ||||||||||
Db         61 PDRFRGSGVGTDFTLTISNLQAELVAVYYCQQYYSTPYSFGQGGRLEI-KRTVAAPSVFI 119

Qy        122 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 179

Qy        182 TLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |   |||||||||||||||||||| ||||||||||
Db        180 TTLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216


RESULT 6
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91131575; PMID:1993660
```

```
A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 <LEO>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             59.3%;  Score 672;  DB 2;  Length 215;
  Best Local Similarity   68.4%;  Pred. No. 1.5e-43;
  Matches  147;  Conservative   16;  Mismatches   48;  Indels    4;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:  :|     :|||  | |:||       ||   ::|| |:|
Db          3 VLTQSPATLSLSPGERATLSGGAS--QSVSSNYLAWYQQKPGQAPRLLIYDASSRATGIP 60

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
               |||||  |    |||:  : || | |:   :  :   ||||||: :  ||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYGQQYGSSPLTFGGGTKVEI-KRTVAAPSVFIF 119

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        120 PPSDEQLKSGTASVVGLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGE 217
              |||||||||||||||| ||||||| |||||||||
Db        180 LTLSKADYEKHKVYAGEVTHQGLSSPVTKSFNRGE 214


RESULT 7
S52059
JC-kappa protein - human
C;Species: Homo sapiens (man)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
C;Accession: S52059
R;Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S.;
EMBO J. 13, 5937-5943, 1994
A;Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy c
A;Reference number: S52059; MUID:95112804; PMID:7813432
A;Accession: S52059
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <FRA>
C;Superfamily: pre-B cell omega light chain; immunoglobulin homology

  Query Match             51.0%;  Score 578.5;  DB 2;  Length 135;
  Best Local Similarity   89.7%;  Pred. No. 1e-36;
  Matches  113;  Conservative    3;  Mismatches    5;  Indels    5;  Gaps    2;

Qy         93 LWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW 152
              ||    | || |||: :  ||||||||||||||||||||||||||||||||||||||||||
Db         15 LW----WTFGQGTKVEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW 69

Qy        153 KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKS 212
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||| |||||
Db         70 KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKLYACEVTHQGLSSPVTKS 129

Qy        213 FNRGEC 218
              ||||||
Db        130 FNRGEC 135


RESULT 8
S06084
Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A;Reference number: S06084; MUID:90016888; PMID:2508067
A;Accession: S06084
A;Molecule type: mRNA
A;Residues: 1-240 <CRO>
A;Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-240/Product: Ig kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>

  Query Match             48.5%;  Score 549.5;  DB 2;  Length 240;
  Best Local Similarity   53.4%;  Pred. No. 2.7e-34;
  Matches  117;  Conservative   24;  Mismatches   73;  Indels    5;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSS---IGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAP 59
              |:||  |:|  | |||||: |:||     :    ||  | |:||      ||   : |
Db         23 VMTQSPSSLAVSAGETVTINCKSSQSLFYSGNQKNYLAWYQQKPGQSPKLLIYWASTRQS 82

Qy         60 GVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSV 119
              ||| || ||  |    |||:  | || | |:|  :|   : || ||||  | |  |||:|
Db         83 GVPDRFIGSGSGTDFTLTISSVQAEDLAIYYCLQYYETPYTFGAGTKLE-LKRADAAPTV 141

Qy        120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
              ||||| ||| :| |||||||:||||||:  |:||:|    :     :|||:|||||||||:
Db        142 SIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGVLDSVTDQDSKDSTYSM 201

Qy        180 SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||:|||||| | :| ||| |:  | || |||||  ||
Db        202 SSTLSLSKADYESHNLYTCEVVHKTSSSPVVKSFNRNEC 240


RESULT 9
PC4402
pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein
C;Species: synthetic
C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C;Accession: PC4402
R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem. 122, 322-329, 1997
A;Title: Construction, bacterial expression, and characterization of hapten-specific si
A;Reference number: PC4402
A;Accession: PC4402
A;Molecule type: DNA
A;Residues: 1-287 <SUZ>
C;Keywords: fusion protein

  Query Match             48.3%;  Score 547.5;  DB 4;  Length 287;
  Best Local Similarity   53.4%;  Pred. No. 4.7e-34;
  Matches  126;  Conservative   14;  Mismatches   49;  Indels   47;  Gaps    6;

Qy          3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         27 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 86

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAP----- 117
              |||||||||||||||||||||| ||||||| | ||||||||||||     |
Db         87 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLSSADDAKKDDAK 146

Qy        118 ------------SVFIFPPSDEQLKSG-TASVVCLLNNFYPREAKVQW----------- 152
                         | :  |  | :| | :  : |  : :      : |
Db        147 KDDAKKDDAKKDGQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEW 206

Qy        153 --KVDNALQSG--------NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC 198
                ::|   ||         |: ::|       : |   |:||       |   || |
Db        207 IGRIDP--NSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLT-----SEDSAVYYC 255


RESULT 10
K3HU
Ig kappa chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S0
R;Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.
```

Biochemistry 9, 3155-3161, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequenc
A;Reference number: A90562; MUID:71064023; PMID:5489770
A;Contents: myeloma protein Eu
A;Accession: B90562
A;Molecule type: protein
A;Residues: 1-106 <GOT>
A;Cross-references: UNIPROT:P01834
A;Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; Eu, disulfide bonds
R;Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
A;Reference number: A91651; MUID:72188439; PMID:5027703
A;Contents: Bence Jones protein Ti
A;Accession: A91651
A;Molecule type: protein
A;Residues: 1-106 <SUT>
R;Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
Cell 22, 197-207, 1980
A;Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv
A;Reference number: A90806; MUID:81042304; PMID:6775818
A;Accession: A90806
A;Molecule type: DNA
A;Residues: 1-106 <HIE>
A;Cross-references: GB:J00241; NID:g33140; PIDN:CAA23823.1; PID:g1335148
A;Note: the sequence was determined from the germline gene
R;Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne,
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,
A;Reference number: A94417
A;Contents: Bence Jones protein Roy
A;Accession: A94417
A;Molecule type: protein
A;Residues: 1-44,'A',46-56,'Q',58-82,'L',84-106 <HIL>
A;Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu
R;Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
A;Title: Die volstaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).
A;Reference number: A91639; MUID:68242259; PMID:5586923
A;Contents: Bence Jones protein Cum
A;Accession: A91639
A;Molecule type: protein
A;Residues: 1-56,'Q',58-106 <HI2>
R;Titani, K.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 244, 3550-3560, 1969
A;Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete
A;Reference number: A92047; MUID:69234734; PMID:4893682
A;Contents: Bence Jones protein Ag
A;Accession: A92047
A;Molecule type: protein
A;Residues: 1-13,'N',15-106 <TIT>
R;Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
Science 169, 56-59, 1970
A;Title: Macroglobulin structure: variable sequence of light and heavy chains.
A;Reference number: A94242; MUID:70201507; PMID:5447531
A;Contents: Waldenstrom's macroglobulin Ou
A;Accession: A94242
A;Molecule type: protein
A;Residues: 1-13,'N',15-106 <KOH>
R;Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
Am. J. Hum. Genet. 48, 613-620, 1991
A;Title: Km typing with PCR: application to population screening.
A;Reference number: A37927; MUID:91150772; PMID:1900145
A;Accession: B37927
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 8-106 <KUR>
A;Note: allotype Inv(3)
R;Steiner, V.; Chang, J.Y.

FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Genetics:
A;Gene: GDB:IGKC
A;Cross-references: GDB:120088; OMIM:147200
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-88/Domain: immunoglobulin homology <IMM>
F;26-86/Disulfide bonds: #status experimental
F;106/Disulfide bonds: interchain (to heavy chain) #status experimental

  Query Match 48.0%; Score 544; DB 1; Length 106;
  Best Local Similarity 99.1%; Pred. No. 3e-34;
  Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 113 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 172
Db 1 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

Qy 173 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
Db 61 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 11
S52450
Ig lambda chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52450
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged gen
A;Reference number: S52445
A;Accession: S52450
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 <BER>
A;Cross-references: EMBL:X82687; NID:g673448; PIDN:CAA58008.1; PID:g673449
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-111/Domain: immunoglobulin homology <IMM>

  Query Match 47.7%; Score 541; DB 2; Length 128;
  Best Local Similarity 96.3%; Pred. No. 6.2e-34;
  Matches 104; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
Db 21 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 80

Qy 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVL 110
Db 81 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 128

RESULT 12
A31790
Ig kappa chain V region (17/9) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: A31790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data for an an
A;Reference number: A92686; MUID:89034213; PMID:3182835

A;Accession: A31790
A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 47.1%; Score 534.5; DB 2; Length 220;
Best Local Similarity 51.6%; Pred. No. 3.4e-33;
Matches 113; Conservative 26; Mismatches 75; Indels 5; Gaps 3;

```
Qy          4 VVTQE-SALTTSPGETVTLTCRSS---IGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAP 59
              |:||  |:|| : || ||::| ||     :    ||  | |:||      ||   : |
Db          3 VMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQQKPGQPPKVLIYWASTRES 62

Qy         60 GVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSV 119
              ||| ||:||  |    |||:  | || | |:|   | |   ||||||| | |  |||:|
Db         63 GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSNPLTFGGGTKLE-LKRADAAPTV 121

Qy        120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
              ||||| ||| || ||||| |||||::  |:||:| : :      | |:|||||||||:
Db        122 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 181

Qy        180 SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||:| :||:|  | || ||:  : |: |||||
Db        182 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 220
```

RESULT 13
L1MS4E
Ig lambda-1 chain precursor V regions (MOPC 104E, RPC20, J558, S104, S178, H2020, S43) -
C;Species: Mus musculus (house mouse)
C;Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004
C;Accession: B93815; B93775; C93775; A93784; B93784; C93784; A90780; C93282; A01995
R;Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A;Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors
A;Reference number: A93815; MUID:77148916; PMID:403522
A;Contents: MOPC 104E
A;Accession: B93815
A;Molecule type: protein
A;Residues: 1-29 <BUR>
A;Cross-references: UNIPROT:P01724
A;Note: this precursor was synthesized in a cell-free system directed by messenger RNA i
d after synthesis
R;Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
A;Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
A;Reference number: A93775; MUID:71107854; PMID:5276767
A;Contents: MOPC 104E; RPC 20
A;Accession: B93775
A;Molecule type: protein
A;Residues: 'Z',21-25,'Q',27-129 <APP>
A;Accession: C93775
A;Molecule type: protein
A;Residues: 20-129 <AP2>
A;Note: compositions and partial sequences of RPC 20 show no differences from MOPC 104E
R;Cesari, I.M.; Weigert, M.
Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
A;Title: Mouse lambda-chain sequences.
A;Reference number: A93784; MUID:73229669; PMID:4516208
A;Contents: J558; S104; S178
A;Accession: A93784
A;Molecule type: protein
A;Residues: 20-129 <CES>
A;Accession: B93784
A;Molecule type: protein
A;Residues: 20-129 <CE2>
A;Accession: C93784
A;Molecule type: protein
A;Residues: 20-43,'N',45-70,'N',72-115,'R',117-129 <CE3>
A;Note: these proteins were isolated from serum or urine of tumor-bearing mice
R;Bernard, O.; Hozumi, N.; Tonegawa, S.
Cell 15, 1133-1144, 1978
A;Title: Sequences of mouse immunoglobulin light chain genes before and after somatic ch
A;Reference number: A90780; MUID:79084170; PMID:103630
A;Contents: H2020
A;Accession: A90780
A;Molecule type: DNA
A;Residues: 1-43,'T',45-50,'G',52-58,'E',60-89,'D',91-129 <BER>
A;Note: the sequence was determined from the differentiated gene
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore,
Nature 298, 380-382, 1982
A;Title: Somatic variants of murine immunoglobulin lambda light chains.
A;Reference number: A93282; MUID:82220143; PMID:6283385
A;Contents: S43
A;Accession: C93282
A;Molecule type: DNA
A;Residues: 1-58,'E',60-89,'D',91-98,'T',100-105,'M',107-129 <BOT>
A;Note: the sequence was determined from the differentiated gene
C;Comment: The MOPC 104E sequence is shown.
C;Genetics:
A;Introns: 16/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; pyroglutamic acid
F;1-19/Domain: signal sequence #status experimental <SIG>
F;20-129/Domain: Ig lambda-1 chain precursor V region #status experimental <MAT>
F;34-111/Domain: immunoglobulin homology <IMM>
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime
F;41-109/Disulfide bonds: #status predicted

Query Match 47.0%; Score 533; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 2.5e-33;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy          3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |||||||||||||||||||||||| ||||||||||||:||||||||||||||||||||
Db         21 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQQKPDHLFTGLIGGTNNRAPGVP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVL 110
              |||||||||:|||||||||||||||| ||||||| | ||||||||||||
Db         81 ARFSGSLIGNKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 128
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RESULT 14
S25058
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: S25058
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
A;Reference number: S25057
A;Accession: S25058
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-235 <FIS>
A;Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-111/Domain: immunoglobulin homology <IMM>

Query Match 46.4%; Score 526; DB 2; Length 235;
Best Local Similarity 50.5%; Pred. No. 1.6e-32;
Matches 109; Conservative 29; Mismatches 72; Indels 6; Gaps 3;

```
Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | :: |||| ||:|| :|    :: :   | |:|        |  |:  | |||
Db         25 VLTQSPAIMSASPGEKVTMTCSAS----SSVSKMQWYQQKSGTSPKRWIYDTSKLASGVP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
              |||||  |   :|||:  : || | |:|  |   |   || ||||  | |  |||:| ||
Db         81 GRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE-LKRADAAPTVSIF 139
```

```
Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||| ||| || ||||| |||||||::  |:||:| : :      | |:|||||||||:|||
Db        140 PPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||:| :||:|  | || ||:  : |: ||||| ||
Db        200 LTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 235


RESULT 15
S06819
Ig lambda chain V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C;Accession: S06819
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06819
A;Molecule type: mRNA
A;Residues: 1-113 <MIL>
A;Cross-references: EMBL:X17168; NID:g52251; PIDN:CAA35046.1; PID:g930172
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-91/Domain: immunoglobulin homology <IMM>
F;21-89/Disulfide bonds: #status predicted

  Query Match             46.3%;  Score 525;  DB 2;  Length 113;
  Best Local Similarity   94.4%;  Pred. No. 8.6e-33;
  Matches  102;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 60

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVL 110
              |||||||||||||||||||||| |||:||| |  ||||||||||
Db         61 ARFSGSLIGDKAALTITGAQTEDEAIYFCSLWYSNHLVFGGGTKLTVL 108


Search completed: June  7, 2005, 16:01:08
Job time : 26 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:37:31 ; Search time 111 Seconds
(without alignments)
1005.705 Million cell updates/sec

Title: US-09-671-953B-7
Perfect score: 1134
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	732	64.6	235	2	Q6GMW0	Q6gmw0 homo sapien
2	731	64.5	235	2	Q6PJF2	Q6pjf2 homo sapien
3	728	64.2	236	2	Q6GMW1	Q6gmw1 homo sapien
4	725	63.9	234	2	Q7Z473	Q7z473 homo sapien
5	722.5	63.7	236	2	Q7Z3Y4	Q7z3y4 homo sapien
6	721	63.6	235	2	Q6GMV9	Q6gmv9 homo sapien
7	720.5	63.5	236	2	Q6GMX9	Q6gmx9 homo sapien
8	720.5	63.5	236	2	Q6PIH7	Q6pih7 homo sapien
9	719.5	63.4	236	2	Q6P5S8	Q6p5s8 homo sapien
10	717.5	63.3	236	2	Q6PIL8	Q6pil8 homo sapien
11	714.5	63.0	236	2	Q6GMX0	Q6gmx0 homo sapien
12	709.5	62.6	236	2	Q6GMX8	Q6gmx8 homo sapien
13	706.5	62.3	236	2	Q6PIH4	Q6pih4 homo sapien
14	699	61.6	236	2	Q6PIT5	Q6pit5 homo sapien
15	695	61.3	240	2	Q6PIH6	Q6pih6 homo sapien
16	692	61.0	239	2	Q8NEK0	Q8nek0 homo sapien
17	692	61.0	239	2	Q8TCD0	Q8tcd0 homo sapien
18	663	58.5	239	2	Q6P491	Q6p491 homo sapien
19	564.5	49.8	120	2	Q6P5R5	Q6p5r5 homo sapien
20	544	48.0	106	1	KAC_HUMAN	P01834 homo sapien
21	539	47.5	129	1	LV1E_MOUSE	P01727 mus musculu
22	534	47.1	129	1	LV1D_MOUSE	P01726 mus musculu
23	533	47.0	129	1	LV1B_MOUSE	P01724 mus musculu
24	527	46.5	129	2	Q8VDE2	Q8vde2 mus musculu
25	525	46.3	110	1	LV1C_MOUSE	P01725 mus musculu
26	518.5	45.7	113	2	Q8CGS1	Q8cgs1 mus musculu
27	516.5	45.5	238	2	Q66JS7	Q66js7 mus musculu
28	512.5	45.2	109	2	Q9ET13	Q9et13 mus musculu
29	505.5	44.6	236	2	Q7TS98	Q7ts98 mus musculu
30	498	43.9	129	1	LV2B_MOUSE	P01729 mus musculu
31	498	43.9	219	2	Q65ZC0	Q65zc0 mus musculu
32	493.5	43.5	241	2	Q63ZX4	Q63zx4 mus musculu
33	478	42.2	117	1	LV1A_MOUSE	P01723 mus musculu
34	450	39.7	117	1	LV2A_MOUSE	P01728 mus musculu
35	441.5	38.9	236	2	Q8NEJ1	Q8nej1 homo sapien
36	440	38.8	235	2	Q6IN99	Q6in99 homo sapien
37	434	38.3	248	2	Q7SYU1	Q7syu1 xenopus lae
38	432.5	38.1	236	2	Q6IPQ0	Q6ipq0 homo sapien
39	430.5	38.0	236	2	Q6PIQ7	Q6piq7 homo sapien
40	430	37.9	233	2	Q8TBC9	Q8tbc9 homo sapien
41	428.5	37.8	230	2	Q7Z2U3	Q7z2u3 homo sapien
42	427.5	37.7	236	2	Q6GMV7	Q6gmv7 homo sapien
43	425.5	37.5	234	2	Q7Z2U7	Q7z2u7 homo sapien
44	424	37.4	231	2	Q6GNB8	Q6gnb8 xenopus lae
45	424	37.4	233	2	Q8N5F4	Q8n5f4 homo sapien

ALIGNMENTS

RESULT 1
Q6GMW0
ID Q6GMW0 PRELIMINARY; PRT; 235 AA.
AC Q6GMW0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

```
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25765 MW;  4360C36B6D4133F5 CRC64;

  Query Match             64.6%;  Score 732;  DB 2;  Length 235;
  Best Local Similarity   70.3%;  Pred. No. 5e-56;
  Matches  154;  Conservative   16;  Mismatches   39;  Indels   10;  Gaps    5;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:||:|    : ||   | |::|      || | ::|  |:|
Db         23 VMTQSPATLSVSPGERATLSCRAS---QSISNNLAWYQQRPGQAPRLLIYGASSRVTGIP 79

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCAL---WYCNLWVFGGGTKLTVLSRTVAAPSV 119
               |||||  | :  |:|:  |:|| | |||     |   |: || |||| :  ||||||||
Db         80 GRFSGSGSGTEFTLSISSLQSEDFAVYFCQQYNDWL--LYTFGQGTKLEI-KRTVAAPSV 136

Qy        120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 196

Qy        180 SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||| ||||||||||
Db        197 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 2
Q6PJF2
ID   Q6PJF2      PRELIMINARY;      PRT;   235 AA.
AC   Q6PJF2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016380; AAH16380.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25520 MW;  F33A145A396BA285 CRC64;

  Query Match             64.5%;  Score 731;  DB 2;  Length 235;
  Best Local Similarity   69.9%;  Pred. No. 6.1e-56;
  Matches  151;  Conservative   19;  Mismatches   42;  Indels    4;  Gaps    3;

Qy          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||  | |: ||||  ||:||:|    : :| |  | |:||      |: |:::|| |:|
Db         23 VLTQSPATLSLSPGERATLSCRAS--QIVSSAYLAWYQQKPGQAPRLLMFGSSSRATGIP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
               |||||  |    |||:  : || | |:|  :  :   || |||: :  ||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSQGTFGPGTKVDI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              ||||||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 3
Q6GMW1
ID   Q6GMW1      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMW1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073791; AAH73791.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
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DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25751 MW;  5BFE6A087AFAC437 CRC64;

  Query Match             64.2%;  Score 728;  DB 2;  Length 236;
  Best Local Similarity   70.0%;  Pred. No. 1.1e-55;
  Matches  154;  Conservative   15;  Mismatches   45;  Indels    6;  Gaps    4;

Qy          1 RSAV-VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              | |: :||  |:|: | |: ||:|||:| |    ||   | |:||       ||   ::
Db         21 RCAIQMTQSPSSLSASVGDRVTITCRASQG---ISNDLGWYQQKPGKAPKLLIYAASSLQ 77

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS 118
               |||:|||||  |    |||:  | || | |:|   |   | || |||: :  |||||||
Db         78 SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYPWTFGQGTKVEI-KRTVAAPS 136

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 196

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||| ||||||||||
Db        197 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 4
Q7Z473
ID   Q7Z473      PRELIMINARY;      PRT;   234 AA.
AC   Q7Z473;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056256; AAH56256.1; -.
DR   HSSP; P01834; 1HEZ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25674 MW;  1A2C259BAB51BC0F CRC64;

  Query Match             63.9%;  Score 725;  DB 2;  Length 234;
  Best Local Similarity   68.2%;  Pred. No. 2e-55;
  Matches  150;  Conservative   19;  Mismatches   45;  Indels    6;  Gaps    4;

Qy          1 RSAV-VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              | |: :||  |: : | |: ||:|||:|    :  :|  | |:||       ||   :
Db         19 RCAIRMTQSPSSFSASTGDRVTITCRAS---QSIGSYLAWYQQKPGKAPQLLIYAASTLQ 75

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS 118
               |||:|||||  |    |:|:  |:|| | |:|  :|   | || |||: :  |||||||
Db         76 SGVPSRFSGSASGTDFTLSISCLQSEDFATYYCQQYYTYPWTFGQGTKVEI-KRTVAAPS 134

Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 194

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||| ||||||||||
Db        195 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234


RESULT 5
Q7Z3Y4
ID   Q7Z3Y4      PRELIMINARY;      PRT;   236 AA.
AC   Q7Z3Y4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
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RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005332; AAH05332.1; -.
DR   HSSP; P01834; 1HEZ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25702 MW;  7FBFE4ED23084BC6 CRC64;

  Query Match             63.7%;  Score 722.5;  DB 2;  Length 236;
  Best Local Similarity   70.2%;  Pred. No. 3.4e-55;
  Matches  151;  Conservative   15;  Mismatches   44;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  |:|: | |:|||:|||:|      |||  | |:||      || | ::   || :
Db         26 MTQSPSSLSASVGDTVTITCRAS---QDISNYLAWFQQKPGKAPKSLIYGASSLQSGVQS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              :|||| |    |||: | || | |:|  :      || |||| :  ||||||||||||
Db         83 KFSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEI-KRTVAAPSVFIFP 141

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 6
Q6GMV9
ID   Q6GMV9      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMV9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073793; AAH73793.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25646 MW;  DF32B580BAD19E4B CRC64;

  Query Match             63.6%;  Score 721;  DB 2;  Length 235;
  Best Local Similarity   69.4%;  Pred. No. 4.6e-55;
  Matches  150;  Conservative   15;  Mismatches   47;  Indels    4;  Gaps    3;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||   |:||:|      | |  | |:||      |:   : || |:|
Db         23 VLTQSPGTLSLSPGERAALSCRAS--QSVNSKYLAWYQQKPGQAPRLLMYAASIRATGIP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
               |||||  |    |||:  ::|| | |||  :  :   ||||||: :  ||||||||||
Db         81 DRFSGSGSGTDFTLTISRLESEDFALYFCQQYGTSPLTFGGGTKVEI-KRTVAAPSVFIF 139

Qy        123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199

Qy        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235


RESULT 7
Q6GMX9
ID   Q6GMX9      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073763; AAH73763.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25924 MW;  FDE2093DC560CFF7 CRC64;

  Query Match             63.5%;  Score 720.5;  DB 2;  Length 236;
  Best Local Similarity   69.3%;  Pred. No. 5.1e-55;
  Matches  149;  Conservative   17;  Mismatches   44;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  |:|: | |  ||:|||:|      | :  | |::|:     ||  |::   |||:
Db         26 MTQSPSSLSASVGHRVTITCRAS---QNVSRWLAWYQQRPEKAPKSLIYATSSLHSGVPS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  |    |||:  | || | |:|  :      ||||||: :  ||||||||||||
Db         83 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNTYPLTFGGGTKVEI-KRTVAAPSVFIFP 141

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 8
Q6PIH7
ID   Q6PIH7      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034141; AAH34141.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25603 MW;  8BC561106861213F CRC64;

  Query Match             63.5%;  Score 720.5;  DB 2;  Length 236;
  Best Local Similarity   70.2%;  Pred. No. 5.1e-55;
  Matches  151;  Conservative   15;  Mismatches   44;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  | |: | |: ||:|||:| |     |:|  | |:||      ||   :    |||:
Db         26 LTQSPSFLSASVGDRVTITCRASQG---ISSYLAWYQQKPGKAPNLLIYAASTLQSGVPS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  |  :   |||:  | || | |:|     :   ||||||: :  ||||||||||||
Db         83 RFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSSPPTFGGGTKVEI-KRTVAAPSVFIFP 141

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 9
Q6P5S8
ID   Q6P5S8      PRELIMINARY;      PRT;   236 AA.
AC   Q6P5S8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062704; AAH62704.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25773 MW;  953E37BEB4FF5F27 CRC64;

  Query Match             63.4%;  Score 719.5;  DB 2;  Length 236;
  Best Local Similarity   69.6%;  Pred. No. 6.3e-55;
  Matches  151;  Conservative   17;  Mismatches   44;  Indels    5;  Gaps    4;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||  ||:||:|      |::  | |::|      || | ::|| |:|
Db         23 VLTQSPGTLSFSPGERATLSCRAS--QTVFSSHLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCN-LWVFGGGTKLTVLSRTVAAPSVFI 121
              |||||  |    ||||  : || | |||  :  :    |||||:: :  |||||||||
Db         81 DRFSGSGSGTDFTLTITRLEPEDFAVYFCQQYGTSPSLTFGGGTRVEI-KRTVAAPSVFI 139

Qy        122 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 199

Qy        182 TLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        200 TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 10
Q6PIL8
ID   Q6PIL8      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIL8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032451; AAH32451.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25834 MW;  6647A9E77A3C0053 CRC64;

  Query Match             63.3%;  Score 717.5;  DB 2;  Length 236;
  Best Local Similarity   69.6%;  Pred. No. 9.4e-55;
  Matches  151;  Conservative   18;  Mismatches   43;  Indels    5;  Gaps    4;

Qy          4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
              |:||    |: ||||  ||:||:|      :|:|  | |:||      || | ::|| |:|
Db         23 VLTQSPGTLSLSPGERATLSCRAS--QSLSSSYLAWYQQKPGQAPRLLIYGVSSRATGIP 80

Qy         63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWV-FGGGTKLTVLSRTVAAPSVFI 121
              |||||  |    |||:  : || | |:|  :  :  : || ||:| :  ||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSRPITFGQGTRLDI-KRTVAAPSVFI 139

Qy        122 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 199

Qy        182 TLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||| ||||||||||
Db        200 TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 11
Q6GMX0
ID   Q6GMX0      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073775; AAH73775.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25807 MW;  864EA08C7E92BF8F CRC64;

  Query Match             63.0%;  Score 714.5;  DB 2;  Length 236;
  Best Local Similarity   69.3%;  Pred. No. 1.7e-54;
  Matches  149;  Conservative   16;  Mismatches   45;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  |:|: | |: ||:|||:|     :|| || | ||      ||   ::   |||:
Db         26 MTQSPSSLSASVGDRVTITCRAS---QNINNYLNWYQLKPGKAPNLLIYAASSLQSGVPS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  |    |||:  : :| | |:|   |     ||||| : :  ||||||||||||
Db         83 RFSGSGSGTDFTLTISSLRPDDFATYYCQQSYNIPLTFGGGTNVEI-KRTVAAPSVFIFP 141

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 12
Q6GMX8
ID   Q6GMX8      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073764; AAH73764.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25707 MW;  4FC8E14B6559EFC9 CRC64;

  Query Match             62.6%;  Score 709.5;  DB 2;  Length 236;
  Best Local Similarity   68.8%;  Pred. No. 4.7e-54;
  Matches  148;  Conservative   19;  Mismatches   43;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  |::: | |: ||:|||:| |     |::  | |:||      ||   ::   |||:
Db         26 MTQSPSSVSASVGDRVTITCRASQG---ISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  |    |||:  | || | |:|    :    : || |||: :  ||||||||||
Db         83 RFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSFPFTFGPGTKVDI-KRTVAAPSVFIFP 141

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
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RESULT 13
Q6PIH4
ID   Q6PIH4      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034146; AAH34146.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25871 MW;  BE01A28CD06EEE26 CRC64;

  Query Match             62.3%;  Score 706.5;  DB 2;  Length 236;
  Best Local Similarity   68.8%;  Pred. No. 8.7e-54;
  Matches  148;  Conservative   18;  Mismatches   44;  Indels    5;  Gaps    3;

Qy          5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
              :||  | |: | |: ||: ||:|      |:  | |:||      ||   :    |||:
Db         26 MTQSPSTLSASVGDRVTIACRAS---QWISDWLAWYQQKPGKAPKLLIYDASRLESGVPS 82

Qy         64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
              |||||  | : :|||:| | :| | |:|  :  |   || |||: :  ||||||||||||
Db         83 RFSGSGSGTEFSLTISGLQPDDFATYYCQPYNSNSPQFGQGTKVEI-KRTVAAPSVFIFP 141

Qy        124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201

Qy        184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||| ||||||||||
Db        202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236


RESULT 14
Q6PIT5
ID   Q6PIT5      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIT5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC029444; AAH29444.1; -.
DR   HSSP; P01607; 1AR2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25741 MW;  BD50AF071FEEE351 CRC64;

  Query Match             61.6%;  Score 699;  DB 2;  Length 236;
  Best Local Similarity   68.6%;  Pred. No. 3.9e-53;
  Matches  151;  Conservative   15;  Mismatches   48;  Indels    6;  Gaps    4;

Qy          1 RSAV-VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
              | |: :||  |:|: | || ||:|||:| |    |:   | |:||      ||   :
Db         21 RCAIQLTQSPSSLSASVGERVTITCRASQG---ISSALAWYQQKPGKPPKLLIYDASTME 77

Qy         59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS 118
              |||:|||||  |    |||:  | || | ::|  :       || || | :  |||||||
Db         78 SGVPSRFSGSGSGTHFTLTISSLQPEDFATFYCQQFKSYPRTFGQGTTLEI-KRTVAAPS 136
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Qy        119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 196

Qy        179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||||||||||| ||||||||||
Db        197 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
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RESULT 15
Q6PIH6
ID Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC034142; AAH34142.1; -.
DR HSSP; P01837; 1KB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;

  Query Match 61.3%; Score 695; DB 2; Length 240;
  Best Local Similarity 69.0%; Pred. No. 9e-53;
  Matches 147; Conservative 17; Mismatches 43; Indels 6; Gaps 4;

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Qy         10 ALTTSPGETVTLTCRSSIGAVTTS--NYANWVQEKPDHLFTGLIGGTNNRAPGVPARFSG 67
              :|: :|||  :::||||   : ::  || :|  :||      ||   :||| ||| ||||
Db         30 SLSVTPGEPASISCRSSQSLLHSNGYNYFDWYLQKPGQSPQLLIYWGSNRASGVPDRFSG 89

Qy         68 SLIGDKAALTITGAQTEDEARYFC--ALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
              | |    | |:  : ||   |:|  ||     : || |||| :  ||||||||||||||
Db         90 SGSGTDFTLKISRVEAEDVGVYYCMQAL-QTPPYTFGQGTKLEI-KRTVAAPSVFIFPPS 147

Qy        126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 207

Qy        186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
              |||||||||||||||||||| |||||||||||
Db        208 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240
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Job time : 112 secs

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